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(54) MORPHOGEN-INDUCED MODULATION OF INFLAMMATORY RESPONSE

Morphogen-induzierte Modulation von entzündlichen Antworten

MODULATION, INDUITE PAR MORPHOGENE, DE REACTION INFLAMMATOIRE

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(74) Representative:

Price, Vincent Andrew et al
FRY HEATH & SPENCE
The Old College
53 High Street
Horley Surrey RH6 7BN (GB)

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WO-A-90/00900 WO-A-91/05802

WO-A-92/07073 WO-A-92/15323

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AL 'OP-1 cDNA encodes an osteogenic protein
in the TGF-beta family'

Remarks:

The file contains technical information submitted
after the application was filed and not included in
this specification

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Description**Field of the Invention**

5 [0001] The present invention relates generally to a method for modulating the inflammatory response induced in a mammal following tissue injury. More particularly, this invention relates to a method for alleviating immune-cell mediated tissue destruction associated with the inflammatory response.

Background of the Invention

10 [0002] The body's inflammatory response to tissue injury can cause significant tissue destruction, leading to loss of tissue function. Damage to cells resulting from the effects of inflammatory response e.g., by immune-cell mediated tissue destruction, has been implicated as the cause of reduced tissue function or loss of tissue function in diseases of the joints (e.g., rheumatoid and osteo-arthritis) and of many organs, including the kidney, pancreas, skin, lung and heart. For example, glomerular nephritis, diabetes, inflammatory bowel disease, vascular diseases such as atherosclerosis and vasculitis, and skin diseases such as psoriasis and dermatitis are believed to result in large part from unwanted acute inflammatory reaction and fibrosis. A number of these diseases, including arthritis, psoriasis and inflammatory bowel disease are considered to be chronic inflammatory diseases. The damaged tissue also often is replaced by fibrotic tissue, e.g., scar tissue, which further reduces tissue function. Graft and transplanted organ rejection also is believed to be primarily due to the action of the body's immune/inflammatory response system.

20 [0003] The immune-cell mediated tissue destruction often follows an initial tissue injury or insult. The secondary damage, resulting from the inflammatory response, often is the source of significant tissue damage. Among the factors thought to mediate these damaging effects are those associated with modulating the body's inflammatory response following tissue injury, e.g., cytokines such as interleukin-1 (IL-1) and tumor necrosis factor (TNF), and oxygen-derived free radicals such as superoxide anions. These humoral agents are produced by adhering neutrophilic leukocytes or by endothelial cells and have been identified at ischemic sites upon reperfusion. Moreover, TNF concentrations are increased in humans after myocardial infarction.

25 [0004] A variety of lung diseases are characterized by airway inflammation, including chronic bronchitis, emphysema, idiopathic pulmonary fibrosis and asthma. Another type of lung-related inflammation disorders are inflammatory diseases characterized by a generalized, wide-spread acute inflammatory response such as adult respiratory distress syndrome. Another dysfunction associated with the inflammatory response is that mounted in response to injury caused by hyperoxia, e.g., prolonged exposure to lethally high concentrations of O₂ (95-100% O₂). Similarly, reduced blood flow to a tissue (and, therefore reduced or lack of oxygen to tissues), as described below, also can induce a primary tissue injury that stimulates the inflammatory response.

30 [0005] It is well known that damage occurs to cells in mammals which have been deprived of oxygen. In fact, the interruption of blood flow, whether partial (hypoxia) or complete (ischemia) and the ensuing inflammatory responses may be the most important cause of coagulative necrosis or cell death in human disease. The complications of atherosclerosis, for example, are generally the result of ischemic cell injury in the brain, heart, small intestines, kidneys, and lower extremities. Highly differentiated cells, such as the proximal tubular cells of the kidney, cardiac myocytes, and the 35 neurons of the central nervous system, all depend on aerobic respiration to produce ATP, the energy necessary to carry out their specialized functions. When ischemia limits the oxygen supply and ATP is depleted, the affected cells may become irreversibly injured. The ensuing inflammatory responses to this initial injury provide additional insult to the affected tissue. Examples of such hypoxia or ischemia are the partial or total loss of blood supply to the body as a whole, an organ within the body, or a region within an organ, such as occurs in cardiac arrest, pulmonary embolus, renal 40 artery occlusion, coronary occlusion or occlusive stroke.

45 [0006] The tissue damage associated with ischemia-reperfusion injury is believed to comprise both the initial cell damage induced by the deprivation of oxygen to the cell and its subsequent recirculation, as well as the damage caused by the body's response to this initial damage. It is thought that reperfusion injury may result in dysfunction to the endothelium of the vasculature as well as injury to the surrounding tissue. In idiopathic pulmonary fibrosis, for example, scar tissue accumulates on the lung tissue lining, inhibiting the tissue's elasticity. The tissue damage associated with 50 hyperoxia injury is believed to follow a similar mechanism, where the initial damage is mediated primarily through the presence of toxic oxygen metabolites followed by an inflammatory response to this initial injury.

55 [0007] Similarly, tissues and organs for transplantation also are subject to the tissue destructive effects associated with the recipient host body's inflammatory response following transplantation. It is currently believed that the initial destructive response is due in large part to reperfusion injury to the transplanted organ after it has been transplanted to the organ recipient.

[0008] Accordingly, the success of organ or tissue transplantation depends greatly on the preservation of the tissue activity (e.g., tissue or organ viability) at the harvest of the organ, during storage of the harvested organ, and at trans-

plantation. To date, preservation of organs such as lungs, pancreas, heart and liver remains a significant stumbling block to the successful transplantation of these organs. U.S. Patent No. 4,952,409 describes a superoxide dismutase-containing liposome to inhibit reperfusion injury. U.S. Patent No. 5,002,965 describes the use of ginkolides, known platelet activating factor antagonists, to inhibit reperfusion injury. Both of these factors are described working primarily by inhibiting the release of and/or inhibiting the damaging effects of free oxygen radicals. A number of patents also have issued on the use of immunosuppressants for inhibiting graft rejection. A representative listing includes U.S. Patent Nos. 5,104,858, 5,008,246 and 5,068,323. A significant problem with many immunosuppressants is their low therapeutic index, requiring the administration of high doses that can have significant toxic side effects.

[0009] Rheumatoid and osteoarthritis are prevalent diseases characterized by chronic inflammation of the synovial membrane lining the afflicted joint. A major consequence of chronic inflammatory joint disease (e.g., rheumatoid arthritis) and degenerative arthritis (e.g., osteoarthritis) is loss of function of those affected joints. This loss of function is due primarily to destruction of the major structural components of the joint, cartilage and bone, and subsequent loss of the proper joint anatomy. As a consequence of chronic disease, joint destruction ensues and can lead to irreversible and permanent damage to the joint and loss of function. Current treatment methods for severe cases of rheumatoid arthritis typically include the removal of the synovial membrane, e.g., synovectomy. Surgical synovectomy has many limitations, including the risk of the surgical procedure itself, and the fact that a surgeon often cannot remove all of the diseased membrane. The diseased tissue remaining typically regenerates, causing the same symptoms which the surgery was meant to alleviate.

[0010] Psoriasis is a chronic, recurrent, scaling skin disease of unknown etiology characterized by chronic inflammation of the skin. Erythematous eruptions, often in papules or plaques, and usually having a white silvery scale, can affect any part of the skin, but most commonly affect the scalp, elbows, knees and lower back. The disease usually occurs in adults, but children may also be affected. Patients with psoriasis have a much greater incidence of arthritis (psoriatic arthritis), and generalized exfoliation and even death can threaten afflicted individuals.

[0011] Current therapeutic regimens include topical or intralesional application of corticosteroids, topical administration of keratolytics, and use of tar and UV light on affected areas. No single therapy is ideal, and it is rare for a patient not to be treated with several alternatives during the relapsing and remitting course of the disease. Whereas systematic treatment can induce prompt resolution of psoriatic lesions, suppression often requires ever-increasing doses, sometimes with toxic side effect, and tapering of therapy may result in rebound phenomena with extensions of lesions, possibly to exfoliation.

[0012] Inflammatory bowel disease (IBD) describes a class of clinical disorders of the gastrointestinal mucosa characterized by chronic inflammation and severe ulceration of the mucosa. The two major diseases in this classification are ulcerative colitis and regional enteritis (Crohn's Disease). Like oral mucositis, the diseases classified as IBD are associated with severe mucosal ulceration (frequently penetrating the wall of the bowel and forming strictures and fistulas), severe mucosal and submucosal inflammation and edema, and fibrosis (e.g., scar tissue formation which interferes with the acid protective function of the gastrointestinal lining.) Other forms of IBD include regional ileitis and proctitis. Clinically, patients with fulminant IBD can be severely ill with massive diarrhea, blood loss, dehydration, weight loss and fever. The prognosis of the disease is not good and frequently requires resection of the diseased tissue.

[0013] The present invention finds application in a method for protecting mammalian tissue, particularly human tissue, from the damage associated with the inflammatory response following a tissue injury. The inflammatory reaction may be in response to an initial tissue injury or insult. The original injury may be chemically, mechanically, biologically or immunologically related. Another application is in methods and compositions for protecting tissue from the tissue destructive effects associated with chronic inflammatory diseases, including arthritis (e.g., rheumatoid or osteoarthritis), psoriatic arthritis, psoriasis and dermatitis, inflammatory bowel disease and other autoimmune diseases. Yet another application is in methods and compositions for enhancing the viability of mammalian tissues and organs to be transplanted, including protecting the transplanted organs from immune cell-mediated tissue destruction, such as the tissue damage associated with ischemia-reperfusion injury. This tissue damage may occur during donor tissue or organ harvesting and transport, as well as following initiation of blood flow after transplantation of the organ or tissue in the recipient host.

[0014] The invention also finds application in a method for alleviating tissue damage associated with ischemic-reperfusion injury in a mammal following a deprivation of oxygen to a tissue in the mammal. Other applications include providing a method for alleviating tissue damage associated with ischemic-reperfusion injury in a human which has suffered from hypoxia or ischemia following cardiac arrest, pulmonary embolus, renal artery occlusion, coronary occlusion or occlusive stroke. A further application is to provide a method for alleviating tissue damage associated with hyperoxia-induced tissue injury, e.g., lethally high oxygen concentrations.

[0015] Still another application of the invention is to provide a method for modulating inflammatory responses in general, particularly those induced in a human following tissue injury.

[0016] These and other objects and features of the invention will be apparent from the description, drawings and claims which follow.

[0017] Each of Kurvilla et al. (1991), 88 Proc. Natl. Acad. Sci. USA 2918-2921, Lefer et al. (1990), 249 Science 61-64; Shepard et. al., EP 0,269,408; Nathan et al., WO90/00900; and, Bentz et al., U.S. Pat. 4,971,952 describe studies testing whether TGF β can mitigate specific types of inflammatory or ischemia reperfusion damage to mammalian cells or tissues. TGF- β is not a member of the class of proteins defined herein as morphogens.

5 [0018] Each of Oppermann et. al., W091/05802; Kuberasampath et al., WO89/09787; Oppermann et al., WO89/09788; and Oppermann et al. W092/07073 teach that OP-1 and related proteins may be used in stimulating tissue-specific regeneration of mammalian cartilage and bone tissue. In particular, these references teach that OP-1, when adsorbed on a suitable supporting matrix, induces the developmental cascade of cellular and molecular events that culminates in endochondral bone morphogenesis. The biologically active OP-1 preparations are taught to be, at
10 best, sparingly soluble in physiologically compatible solutions. OP-1-charged matrix devices thus are disclosed as useful for inducing local morphogenesis of bone and/or cartilage.

[0019] Cohen et al., W092/15323 teaches that OP-1 induces tissue specific morphogenesis in diverse mammalian body tissues, and that morphogen can be used in the replacement or repair of damaged tissues.

15 **Summary of the Invention**

[0020] The present invention is defined in the claims. It finds utility in a method for alleviating the tissue destructive effects associated with activation of the inflammatory response following tissue injury. The method comprises the step of providing to the affected tissue a therapeutically effective concentration of a morphogenic protein ("morphogen", as defined herein) upon tissue injury or in anticipation of tissue injury, sufficient to substantially inhibit or reduce the tissue destructive effects of the inflammatory response.

20 [0021] Also described herein are compositions and therapeutic treatment methods that comprise the step of administering to a mammal a therapeutically effective amount of a morphogenic protein ("morphogen"), as defined herein, upon injury to a tissue, or in anticipation of such injury, for a time and at a concentration sufficient to inhibit the tissue destructive effects associated with the body's inflammatory response, including repairing damaged tissue, and/or inhibiting additional damage thereto.

25 [0022] Also described herein are compositions and therapeutic treatment methods for protecting tissues and organs from the tissue destructive effects of the inflammatory response which include administering to the mammal, upon injury to a tissue or in anticipation of such injury, a compound that stimulates in vivo a therapeutically effective concentration of an endogenous morphogen within the body of the mammal sufficient to protect the tissue from the tissue destructive effects associated with the inflammatory response, including repairing damaged tissue and/or inhibiting additional damage thereto. These compounds are referred to herein as morphogen-stimulating agents, and are understood to include substances which, when administered to a mammal, act on cells of tissue(s) or organ(s) that normally are responsible for, or capable of, producing a morphogen and/or secreting a morphogen, and which cause the endogenous level of the morphogen to be altered. The agent may act, for example, by stimulating expression and/or secretion of an endogenous morphogen.

30 [0023] As embodied herein, the term "ischemic-reperfusion injury" refers to the initial damage associated with oxygen deprivation of a cell and the subsequent damage associated with the inflammatory response when the cell is resupplied with oxygen. As embodied herein, the term "hyperoxia-induced injury" refers to the tissue damage associated with prolonged exposure to lethally high doses of oxygen, e.g., greater than 95% O₂, including the tissue damage associated with the inflammatory response to the toxicologically high oxygen dose. Accordingly, as used herein, "toxic oxygen concentrations" refers to the tissue damage associated with the injury induced by both lethally low oxygen concentrations of oxygen (including a complete lack of oxygen), and by lethally high oxygen concentrations. The expression "alleviating" means the protection from, reduction of and/or elimination of undesired tissue destruction, particularly immune cell-mediated tissue destruction. The tissue destruction may be in response to an initial tissue injury, which may be mechanical, chemical or immunological in origin. The expression "enhance the viability of" living tissues or organs, as used herein, means protection from, reduction of and/or elimination of reduced or lost tissue or organ function as a result of tissue death, particularly immune cell-mediated tissue death. "Transplanted" living tissue encompasses both tissue transplants (e.g., as in the case of bone marrow transplants) and tissue grafts. Finally, a "free oxygen radical inhibiting agent" means a molecule capable of inhibiting the release of and/or inhibiting tissue damaging effects of free oxygen radicals.

35 [0024] Described herein are methods and compositions for alleviating the ischemic-reperfusion injury in mammalian tissue resulting from a deprivation of, and subsequent reperfusion of, oxygen to the tissue. Also described is a method for alleviating the tissue-destructive effects associated with hyperoxia. Methods and compositions for maintaining the viability of tissues and organs, particularly living tissues and organs to be transplanted, including protecting them from ischemia-reperfusion injury, together with methods for protecting tissues and organs from the tissue destructive effects of chronic inflammatory diseases, such as arthritis, psoriasis, dermatitis, including contact dermatitis, IBD and other chronic inflammatory diseases of the gastrointestinal tract, as well as the tissue destructive effects associated

with other, known autoimmune diseases, such as diabetes, multiple sclerosis, amyotrophic lateral sclerosis (ALS), and other autoimmune neurodegenerative diseases are also described herein.

[0025] The morphogen may be provided to the damaged tissue following an initial injury to the tissue. The morphogen may be provided directly to the tissue, as by injection to the damaged tissue site or by topical administration, or 5 may be provided indirectly, e.g., systemically by oral or parenteral means. Alternatively, as described above, an agent capable of stimulating endogenous morphogen expression and/or secretion may be administered to the mammal. Preferably, the agent can stimulate an endogenous morphogen in cells associated with the damaged tissue. Alternatively, morphogen expression and/or secretion may be stimulated in a distant tissue and the morphogen transported to the damaged tissue by the circulatory system.

10 [0026] The morphogen may also be provided to tissue at risk of damage due to immune cell-mediated tissue destruction. Examples of such tissues include tissue grafts and tissue or organ transplants, as well as any tissue or organ about to undergo a surgical procedure or other clinical procedure likely to either inhibit blood flow to the tissue or otherwise induce an inflammatory response. Here the morphogen or morphogen-stimulating agent preferably is provided to the patient prior to induction of the injury, e.g., as a prophylactic, to provide a cyto-protective effect to the tissue 15 at risk.

20 [0027] Where the tissue at risk comprises a tissue or organ to be transplanted, the tissue or organ to be transplanted preferably is exposed to a morphogen prior to transplantation. Most preferably, the tissue or organ is exposed to the morphogen prior to its removal from the donor, by providing the donor with a composition comprising a morphogen or morphogen-stimulating agent. Alternatively or, in addition, once removed from the donor, the organ or tissue is placed in a preservation solution containing a morphogen or morphogen-stimulating agent. In addition, the recipient 25 also preferably is provided with a morphogen or morphogen-stimulating agent just prior to, or concomitant with, transplantation. In all cases, the morphogen or morphogen-stimulating agent may be administered directly to the tissue at risk, as by injection or topical administration to the tissue, or it may be provided systemically, either by oral or parenteral administration.

25 [0028] The morphogens described herein are envisioned to be useful in enhancing viability of any organ or living tissue to be transplanted. The morphogens may be used to particular advantage in lung, heart, liver, kidney or pancreas transplants, as well as in transplantation and/or grafting of bone marrow, skin, gastrointestinal mucosa, and other living tissues.

30 [0029] Where the patient suffers from a chronic inflammatory disease, such as diabetes, arthritis, psoriasis, IBD, and the like, the morphogen or morphogen-stimulating agent preferably is administered at regular intervals as a prophylactic, to prevent and/or inhibit the tissue damage normally associated with the disease during flare periods. As above, the morphogen or morphogen-stimulating agent may be provided directly to the tissue at risk, for example by injection or by topical administration, or indirectly, as by systemic e.g., oral or parenteral administration.

35 [0030] Among the morphogens useful in this invention are proteins originally identified as osteogenic proteins, such as the OP-1, OP-2 and CBMP2 proteins, as well as amino acid sequence-related proteins such as DPP (from *Drosophila*), Vgl (from *Xenopus*), Vgr-1 (from mouse, see U.S. 5,011,691 to Oppermann et al.), GDF-1 (from mouse, see Lee (1991) *PNAS* 88:4250-4254), all of which are presented in Table II and Seq. ID Nos.5-14), and the recently identified 60A protein (from *Drosophila*, Seq. ID No. 24, see Wharton et al. (1991) *PNAS* 88:9214-9218.) The members of 40 this family, which include members of the TGF- β super-family of proteins, share substantial amino acid sequence homology in their C-terminal regions. The proteins are translated as a precursor, having an N-terminal signal peptide sequence, typically less than about 30 residues, followed by a "pro" domain that is cleaved to yield the mature sequence. The signal peptide is cleaved rapidly upon translation, at a cleavage site that can be predicted in a given sequence using the method of Von Heijne ((1986) *Nucleic Acids Research* 14:4683-4691.) Table I, below, describes the various morphogens identified to date, including their nomenclature as used herein, their Seq. ID references, and publication sources for the amino acid sequences for the full length proteins not included in the Seq. Listing.

TABLE I

50 "OP-1" Refers generically to the group of
 morphogenically active proteins expressed
 from part or all of a DNA sequence
 encoding OP-1 protein, including allelic
 and species variants thereof, e.g., human

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5 OP-1 ("hOP-1", Seq. ID No. 5, mature
protein amino acid sequence), or mouse
10 OP-1 ("mOP-1", Seq. ID No. 6, mature
protein amino acid sequence.) The
conserved seven cysteine skeleton is
defined by residues 38 to 139 of Seq. ID
Nos. 5 and 6. The cDNA sequences and the
amino acids encoding the full length
15 proteins are provided in Seq. ID Nos. 16
and 17 (hOP1) and Seq. ID Nos. 18 and 19
(mOP1.) The mature proteins are defined
by residues 293-431 (hOP1) and 292-430
20 (mOP1). The "pro" regions of the
proteins, cleaved to yield the mature,
morphogenically active proteins are
defined essentially by residues 30-292
25 (hOP1) and residues 30-291 (mOP1).

30 "OP-2" refers generically to the group of active
proteins expressed from part or all of a
DNA sequence encoding OP-2 protein,
including allelic and species variants
35 thereof, e.g., human OP-2 ("hOP-2", Seq.
ID No. 7, mature protein amino acid
sequence) or mouse OP-2 ("mOP-2", Seq. ID
No. 8, mature protein amino acid
sequence). The conserved seven cysteine
40 skeleton is defined by residues 38 to 139
of Seq. ID Nos. 7 and 8. The cDNA
sequences and the amino acids encoding the
full length proteins are provided in Seq.
45 ID Nos. 20 and 21 (hOP2) and Seq. ID Nos.
22 and 23 (mOP2.) The mature proteins are
50 defined essentially by residues 264-402
(hOP2) and 261-399 (mOP2). The "pro"

regions of the proteins, cleaved to yield the mature, morphogenically active proteins likely are defined essentially by residues 18-263 (*hOP2*) and residues 18-260 (*mOP2*). (Another cleavage site also occurs 21 residues upstream for both OP-2 proteins.)

"CBMP2" refers generically to the morphogenically active proteins expressed from a DNA sequence encoding the CBMP2 proteins, including allelic and species variants thereof, e.g., human CBMP2A ("CBMP2A(fx)", Seq ID No. 9) or human CBMP2B DNA ("CBMP2B(fx)", Seq. ID No. 10). The amino acid sequence for the full length proteins, referred to in the literature as BMP2A and BMP2B, or BMP2 and BMP4, appear in Wozney, et al. (1988) Science 242:1528-1534. The pro domain for BMP2 (BMP2A) likely includes residues 25-248 or 25-282; the mature protein, residues 249-396 or 283-396. The pro domain for BMP4 (BMP2B) likely includes residues 25-256 or 25-292; the mature protein, residues 257-408 or 293-408.

"DPP(fx)" refers to protein sequences encoded by the Drosophila DPP gene and defining the conserved seven cysteine skeleton (Seq. ID No. 11). The amino acid sequence for the full length protein appears in Padgett, et

5 al (1987) Nature 325: 81-84. The pro
domain likely extends from the signal
peptide cleavage site to residue 456; the
mature protein likely is defined by
residues 457-588.

10 "Vgl(fx)" refers to protein sequences encoded by the
Xenopus Vgl gene and defining the
conserved seven cysteine skeleton (Seq. ID
No. 12). The amino acid sequence for the
full length protein appears in
Weeks (1987) Cell 51: 861-867. The
prodomain likely extends from the signal
peptide cleavage site to residue 246; the
mature protein likely is defined by
residues 247-360.

15 "Vgr-1(fx)" refers to protein sequences encoded by the
murine Vgr-1 gene and defining the
conserved seven cysteine skeleton (Seq. ID
No. 13). The amino acid sequence for the
full length protein appears in Lyons, et
al, (1989) PNAS 86: 4554-4558. The
prodomain likely extends from the signal
peptide cleavage site to residue 299; the
mature protein likely is defined by
residues 300-438.

20 "GDF-1(fx)" refers to protein sequences encoded by the
human GDF-1 gene and defining the
conserved seven cysteine skeleton (Seq. ID
No. 14). The cDNA and encoded amino
sequence for the full length protein is

5 provided in Seq. ID. No. 32. The prodomain likely extends from the signal peptide cleavage site to residue 214; the mature protein likely is defined by residues 215-372.

10 "60A" refers generically to the morphogenically active proteins expressed from part or all of a DNA sequence (from the Drosophila 60A gene) encoding the 60A proteins (see Seq. ID No. 24 wherein the cDNA and encoded amino acid sequence for the full length protein is provided). "60A(fx)" refers to the protein sequences defining the conserved seven cysteine skeleton (residues 354 to 455 of Seq. ID No. 24.)
15 The prodomain likely extends from the signal peptide cleavage site to residue 324; the mature protein likely is defined by residues 325-455.
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"BMP3(fx)" refers to protein sequences encoded by the human BMP3 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 26). The amino acid sequence for the full length protein appears in Wozney et al. (1988) Science 242: 1528-1534. The pro domain likely extends from the signal peptide cleavage site to residue 290; the mature protein likely is defined by residues 291-472.
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5 **"BMP5(fx)"** refers to protein sequences encoded by the
 human BMP5 gene and defining the conserved
 seven cysteine skeleton (Seq. ID No. 27).
 The amino acid sequence for the full
 length protein appears in Celeste, et al.
 10 (1991) PNAS 87: 9843-9847. The pro domain
 likely extends from the signal peptide
 cleavage site to residue 316; the mature
 protein likely is defined by residues
 15 317-454.

20 **"BMP6(fx)"** refers to protein sequences encoded by the
 human BMP6 gene and defining the conserved
 seven cysteine skeleton (Seq. ID No. 28).
 The amino acid sequence for the full
 length protein appears in Celeste, et al.
 25 (1990) PNAS 87: 9843-5847. The pro domain
 likely includes extends from the signal
 peptide cleavage site to residue 374; the
 mature sequence likely includes
 30 residues 375-513.

35 **[0031]** The OP-2 proteins have an additional cysteine residue in this region (e.g., see residue 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The GDF-1 protein has a four amino acid insert within the conserved skeleton (residues 44-47 of Seq. ID No. 14) but this insert likely does not interfere with the relationship of the cysteines in the folded structure. In addition, the CBMP2 proteins are missing one amino acid residue within the cysteine skeleton.

40 **[0032]** The morphogens are inactive when reduced, but are active as oxidized homodimers and when oxidized in combination with other morphogens of this invention (e.g., as heterodimers). Thus, as defined herein, a morphogen is a dimeric protein comprising a pair of polypeptide chains, wherein each polypeptide chain comprises at least the C-terminal six cysteine skeleton defined by residues 43-139 of Seq. ID No. 5, including functionally equivalent arrangements of these cysteines (e.g., amino acid insertions or deletions which alter the linear arrangement of the cysteines in the sequence but not their relationship in the folded structure), such that, when the polypeptide chains are folded, the dimeric protein species comprising the pair of polypeptide chains has the appropriate three-dimensional structure, including the appropriate intra-or inter-chain disulfide bonds such that the protein is capable of acting as a morphogen as defined herein. Specifically, the morphogens generally are capable of all of the following biological functions in a

45 morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. In addition, it is also anticipated that these morphogens are capable of inducing redifferentiation of committed cells under appropriate environmental conditions.

50 **[0033]** In one preferred aspect, the morphogens of this invention comprise one of two species of generic amino acid sequences: Generic Sequence 1 (Seq. ID No. 1) or Generic Sequence 2 (Seq. ID No. 2); where each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof. Generic Sequence 1 comprises the conserved six cysteine skeleton and Generic Sequence 2 comprises the conserved six cysteine skeleton plus the additional cysteine identified in OP-2 (see residue 36, Seq. ID No. 2). In another preferred aspect, these sequences further

comprise the following additional sequence at their N-terminus:

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)

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[0034] Preferred amino acid sequences within the foregoing generic sequences include: Generic Sequence 3 (Seq. ID No. 3), Generic Sequence 4 (Seq. ID No. 4), Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31), listed below. These Generic Sequences accommodate the homologies shared among the various preferred members of this morphogen family identified in Table II, as well as the amino acid sequence variation among them. Specifically, Generic Sequences 3 and 4 are composite amino acid sequences of the following proteins presented in Table II and identified in Seq. ID Nos. 5-14: human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from *Drosophila*, Seq. ID No. 11), Vgl, (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14.) The generic sequences include both the amino acid identity shared by the sequences in Table II, as well as alternative residues for the variable positions within the sequence. Note that these generic sequences allow for an additional cysteine at position 41 or 46 in Generic Sequences 3 or 4, respectively, providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins.

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Generic Sequence 3

Leu Tyr Val Xaa Phe

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Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

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10

Xaa Ala Pro Xaa Gly Xaa Xaa Ala

15 20

15

Xaa Tyr Cys Xaa Gly Xaa Cys Xaa

25 30

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Xaa Pro Xaa Xaa Xaa Xaa Xaa

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Xaa Xaa Xaa Asn His Ala Xaa Xaa

25

40 45

Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa

50

30

Xaa Xaa Xaa Xaa Xaa Xaa Cys

55 60

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Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

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Xaa Xaa Xaa Leu Xaa Xaa Xaa

70 75

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Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

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Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85 90

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Xaa Cys Gly Cys Xaa

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wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows:
 "Res." means "residue" and Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser or Lys); Xaa at res.7 = (Asp or Glu); Xaa at res.8 = (Leu or Val); Xaa at res.11 = (Gln, Leu, Asp, His or Asn); Xaa at res.12 = (Asp, Arg or Asn); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Leu or Gln); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at res.26 = (Glu, His, Tyr, Asp or Gln); Xaa at res.28 = (Glu, Lys, Asp or Gln); Xaa at res.30 = (Ala, Ser, Pro or Gln); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu or Val); Xaa at res.34 = (Asn, Asp, Ala or Thr); Xaa at res.35 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn or Ser); Xaa at res.39 = (Ala, Ser or Gly); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile or Val); Xaa at res.45 = (Val or Leu); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His or Asn); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala or Val); Xaa at res.53 = (Asn, Lys, Ala or Glu); Xaa at res.54 = (Pro or Ser); Xaa at res.55 = (Glu, Asp, Asn, or Gly); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys or Leu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr or Ala); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser or Asp); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr or Val); Xaa at res.71 = (Ser or Ala); Xaa at res.72 = (Val or Met); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr or Leu); Xaa at res.76 = (Asp or Asn); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn or Tyr); Xaa at res.79 = (Ser, Asn, Asp or Glu); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile or Val); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln or His); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln or Glu); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr or Ala); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly or Glu); and Xaa at res.97 = (His or Arg);

Generic Sequence 4

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Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
1					5				10
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
					15				
Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala		
	20					25			
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
			30			35			

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	Xaa Pro Xaa Xaa Xaa Xaa Xaa	
		40
5	Xaa Xaa Xaa Asn His Ala Xaa Xaa	
		45
	Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa	
		55
10	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys	
		60
	Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa	
		70
	Xaa Xaa Xaa Leu Xaa Xaa Xaa	
		75
20	Xaa Xaa Xaa Xaa Val Xaa Leu Xaa	
		85
	Xaa Xaa Xaa Xaa Met Xaa Val Xaa	
		90
25	Xaa Cys Gly Cys Xaa	
		100

30 wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys or Arg); Xaa at res.3 = (Lys or Arg); Xaa at res.4 = (His or Arg); Xaa at res.5 = (Glu, Ser, His, Gly, Arg or Pro); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser or Lys); Xaa at res.12 = (Asp or Glu); Xaa at res.13 = (Leu or Val); Xaa at res.16 = (Gln, Leu, Asp, His or Asn); Xaa at res.17 = (Asp, Arg, or Asn); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Leu, or Gln); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp or Gln); Xaa at res.33 = (Glu, Lys, Asp or Gln); Xaa at res.35 = (Ala, Ser or Pro); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu or Val); Xaa at res.39 = (Asn, Asp, Ala or Thr); Xaa at res.40 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.44 = (Ala, Ser or Gly); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile or Val); Xaa at res.50 = (Val or Leu); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His or Asn); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala or Val); Xaa at res.58 = (Asn, Lys, Ala or Glu); Xaa at res.59 = (Pro or Ser); Xaa at res.60 = (Glu, Asp, or Gly); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys or Leu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr or Ala); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser or Asp); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr or Val); Xaa at res.76 = (Ser or Ala); Xaa at res.77 = (Val or Met); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr or Leu); Xaa at res.81 = (Asp or Asn); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn or Tyr); Xaa at res.84 = (Ser, Asn, Asp or Glu); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile or Val); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln or His); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln or Glu); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr or Ala); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly or Glu); and Xaa at res.102 = (His or Arg).

55 [0035] Similarly, Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31) accommodate the homologies shared among all the morphogen protein family members identified in Table II. Specifically, Generic Sequences 5 and 6 are composite amino acid sequences of human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14), human BMP3 (Seq. ID No. 26), human BMP5 (Seq. ID No. 27), human BMP6 (Seq. ID No. 28) and 60(A) (from Drosophila, Seq. ID Nos. 24-25). The generic

sequences include both the amino acid identity shared by these sequences in the C-terminal domain, defined by the six and seven cysteine skeletons (Generic Sequences 5 and 6, respectively), as well as alternative residues for the variable positions within the sequence. As for Generic Sequences 3 and 4, Generic Sequences 5 and 6 allow for an additional cysteine at position 41 (Generic Sequence 5) or position 46 (Generic Sequence 6), providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and containing certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 5

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Leu Xaa Xaa Xaa Phe

1 5

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Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

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Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Ala
15					20		
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa
			25				30
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	
				35			
Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa
			40				45
Xaa							
				50			
Xaa	Cys						
			55				60
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa
				65			
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	
70					75		
Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa
				80			
Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa
85					90		
Xaa	Cys	Xaa	Cys	Xaa			
					95		

45 wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows:
"Res." means "residue" and Xaa at res.2 = (Tyr or Lys); Xaa at res.3 = Val or Ile); Xaa at res.4 = (Ser, Asp or Glu); Xaa
at res.6 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.7 = (Asp, Glu or Lys); Xaa at res.8 = (Leu, Val or Ile); Xaa at res.11 =
50 (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.12 = (Asp, Arg, Asn or Glu); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile
or Val); Xaa at res.16 (Ala or Ser); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.19 = (Gly or Ser); Xaa at
res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Gln, Leu or Gly); Xaa at res.23 = (Tyr, Asn or Phe); Xaa
at res.26 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.28 = (Glu, Lys, Asp, Gln or Ala); Xaa at res.30 = (Ala, Ser, Pro,
55 Gln or Asn); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu, Val or Met); Xaa at res.34 = (Asn, Asp, Ala, Thr or
Pro); Xaa at res.35 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met,
Phe, Gly or Leu); Xaa at res.38 = (Asn, Ser or Lys); Xaa at res.39 = (Ala, Ser, Gly or Pro); Xaa at res.40 = (Thr, Leu or
Ser); Xaa at res.44 = (Ile, Val or Thr); Xaa at res.45 = (Val, Leu or Ile); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr,
60 Ala or Ser); Xaa at res.48 = (Leu or Ile); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His, Asn or Arg); Xaa at res.51 =
(Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.53 = (Asn, Lys, Ala, Glu, Gly

or Phe); Xaa at res.54 = (Pro, Ser or Val); Xaa at res.55 = (Glu, Asp, Asn, Gly, Val or Lys); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys, Leu or Glu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr, Ala or Glu); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser, Asp or Gly); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr, Val or Leu); Xaa at res.71 = (Ser, Ala or Pro); Xaa at res.72 = (Val, Met or Ile); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr, Leu or His); Xaa at res.76 = (Asp, Asn or Leu); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.79 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile, Val or Asn); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln, His or Val); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln, Glu or Pro); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr, Ala or Ile); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly, Glu or Ser); Xaa at res.95 = (Gly or Ala) and Xaa at res.97 = (His or Arg).

Generic Sequence 6

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Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
 1 5 10

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Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
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Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
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Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
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Xaa Pro Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Asn His Ala Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65

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Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 70

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Xaa Xaa Xaa Leu Xaa Xaa Xaa		
5	75	80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa		
85		
Xaa Xaa Xaa Xaa Met Xaa Val Xaa		
10	90	95
Xaa Cys Xaa Cys Xaa		
100		

15 wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys, Arg, Ala or Gln); Xaa at res.3 = (Lys, Arg or Met); Xaa at res.4 = (His, Arg or Gln); Xaa at res.5 = (Glu, Ser, His, Gly, Arg, Pro, Thr, or Tyr); Xaa at res.7 = (Tyr or Lys); Xaa at res.8 = (Val or Ile); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.12 = (Asp, Glu, or Lys); Xaa at res.13 = (Leu, Val or Ile); Xaa at res.16 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.17 = (Asp, Arg, Asn or Glu); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.21 = (Ala or Ser); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.24 = (Gly or Ser); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Gln, Leu, or Gly); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.33 = (Glu, Lys, Asp, Gln or Ala); Xaa at res.35 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu, Val or Met); Xaa at res.39 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.40 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.43 = (Asn, Ser or Lys); Xaa at res.44 = (Ala, Ser, Gly or Pro); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile, Val or Thr); Xaa at res.50 = (Val, Leu or Ile); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.53 = (Leu or Ile); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His, Asn or Arg); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.58 = (Asn, Lys, Ala, Glu, Gly or Phe); Xaa at res.59 = (Pro, Ser or Val); Xaa at res.60 = (Glu, Asp, Gly, Val or Lys); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys, Leu or Glu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr, Ala or Glu); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser, Asp or Gly); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr, Val or Leu); Xaa at res.76 = (Ser, Ala or Pro); Xaa at res.77 = (Val, Met or Ile); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr, Leu or His); Xaa at res.81 = (Asp, Asn or Leu); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.84 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile, Val or Asn); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln, His or Val); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln, Glu or Pro); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr, Ala or Ile); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly, Glu or Ser); Xaa at res.100 = (Gly or Ala); and Xaa at res.102 = (His or Arg).

45 [0036] Particularly useful sequences for use as morphogens in this invention include the C-terminal domains, e.g., the C-terminal 96-102 amino acid residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B, GDF-1 (see Table II, below, and Seq. ID Nos. 5-14), as well as proteins comprising the C-terminal domains of 60A, BMP3, BMP5 and BMP6 (see Seq. ID Nos. 24-28), all of which include at least the conserved six or seven cysteine skeleton. In addition, biosynthetic constructs designed from the generic sequences, such as COP-1, 3-5, 7, 16, disclosed in U.S. Pat. No. 5,011,691, also are useful. Other sequences include the inhibins/activin proteins (see, for example, U.S. Pat. Nos. 4,968,590 and 5,011,691). Accordingly, other useful sequences are those sharing at least 70% amino acid sequence homology or "similarity", and preferably 80% homology or similarity with any of the sequences above. These are anticipated to include allelic and species variants and mutants, and biosynthetic muteins, as well as novel members of this morphogenic family of proteins. Particularly envisioned in the family of related proteins are those proteins exhibiting morphogenic activity and wherein the amino acid changes from the preferred sequences include conservative changes, e.g., those as defined by Dayoff et al., *Atlas of Protein Sequence and Structure*; vol. 5, Suppl. 3, pp. 345-362, (M.O. Dayoff, ed., Nat'l BioMed. Research Fdn., Washington, D.C. 1979). As used herein, potentially useful sequences are 50 aligned with a known morphogen sequence using the method of Needleman et al. ((1970) *J.Mol.Biol.* 48:443-453) and identities calculated by the Align program (DNAstar, Inc.). "Homology" or "similarity" as used herein includes allowed conservative changes as defined by Dayoff et al.

55 [0037] The currently most preferred protein sequences useful as morphogens in this invention include those having

greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the *Drosophila* 60A protein. Accordingly, in another preferred aspect of the invention, useful morphogens include active proteins comprising species of polypeptide chains having the generic amino acid sequence herein referred to as "OPX", which accommodates the homologies between the various identified species of OP1 and OP2 (Seq. ID No. 29).

[0038] The morphogens useful in the methods, composition and devices of this invention include proteins comprising any of the polypeptide chains described above, whether isolated from naturally-occurring sources, or produced by recombinant DNA or other synthetic techniques, and includes allelic and species variants of these proteins, naturally-occurring or biosynthetic mutants thereof, as well as various truncated and fusion constructs. Deletion or addition mutants also are envisioned to be active, including those which may alter the conserved C-terminal cysteine skeleton, provided that the alteration does not functionally disrupt the relationship of these cysteines in the folded structure. Accordingly, such active forms are considered the equivalent of the specifically described constructs disclosed herein.

[0039] The proteins may include forms having varying glycosylation patterns, varying N-termini, a family of related proteins having regions of amino acid sequence homology, and active truncated or mutated forms of native or biosynthetic proteins, produced by expression of recombinant DNA in host cells.

[0040] The morphogenic proteins can be expressed from intact or truncated cDNA or from synthetic DNAs in prokaryotic or eucaryotic host cells, and purified, cleaved, refolded, and dimerized to form morphogenically active compositions. Currently preferred host cells include *E. coli* or mammalian cells, such as CHO, COS or BSC cells. A detailed description of the morphogens useful in the methods, compositions and devices of this invention is disclosed in copending US patent application Serial Nos. 752,764, filed August 30, 1991, and 667,274, filed March 11, 1991.

[0041] Thus, in view of this disclosure, skilled genetic engineers can isolate genes from cDNA or genomic libraries of various different species which encode appropriate amino acid sequences, or construct DNAs from oligonucleotides, and then can express them in various types of host cells, including both prokaryotes and eucaryotes, to produce large quantities of active proteins capable of protecting tissues and organs from immune cell-mediated tissue destruction, including substantially inhibiting such damage and/or regenerating the damaged tissue in a variety of mammals, including humans.

[0042] The foregoing and other objects, features and advantages of the present invention will be made more apparent from the following detailed description of the invention.

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Brief Description of the Drawings

[0043]

- 35 FIG 1 shows the cardioprotective effects of morphogen (hOP1) in a rat myocardial ischemia-reperfusion model, as evidenced by the smaller loss of myocardial creatine kinase in hOP1-treated rats;
- FIG 2 shows the effects of 20 µg of morphogen (hOP1 given 24 hours prior to isolation of rat heart on endothelial-dependent vasorelaxation to acetylcholine following induced ischemia-reperfusion injury;
- 40 FIG 3 shows the effect of morphogen (hOP1) on neutrophil adherence to LTB₄-stimulated mesenteric artery endothelium in neutrophil-activated rats;
- FIG 4 (A and B) are schematic representations of morphogen inhibition of early mononuclear phagocytic multinuclearization *in vivo*;
- 45 FIG 5 graphs the effect of a morphogen (e.g., OP-1) and a placebo control on mucositis lesion formation; and
- FIG 6 (A-D) graphs the effects of a morphogen (eg., OP-1, Figs. 6A and 6C) and TGF-β (Fig. 6B and 6D) on collagen (6A and 6B) and hyaluronic acid (6C and 6D) production in primary fibroblast cultures.

Detailed Description of the Invention

[0044] It now has been surprisingly discovered that the morphogens defined herein are effective agents in alleviating the tissue destructive effects associated with the body's inflammatory response to tissue injury. In particular, as disclosed herein, the morphogens are capable of alleviating the necrotic tissue effects associated with the ensuing inflammatory responses that occur following an initial tissue injury.

[0045] When tissue injury occurs, whether caused by bacteria, trauma, chemicals, heat, or any other phenomenon,

the body's inflammatory response is stimulated. In response to signals released from the damaged cells (e.g., cytokines), extravascularization of immune effector cells is induced. Under ordinary circumstances these invading immune effector cells kill the infectious agent and/or infected or damaged cells (through the release of killing substances such as superoxides, perforins, and other antimicrobial agents stored in granules), remove the dead tissues and organisms (through phagocytosis), release various biological response modifiers that promote rapid healing and covering of the wound (quite often resulting in the formation of fibrotic scar tissue), and then, after the area is successfully healed, exit from the site of the initial insult. Once the site is perceived to be normal, the local release of inflammatory cytokines ceases and the display of adhesion molecules on the vessel endothelium returns to basal levels. In some cases, however, the zeal of these interacting signals and cellular systems, which are designed to capture and contain very rapidly multiplying infectious agents, act to the detriment of the body, killing additional, otherwise healthy, surrounding tissue. This additional unnecessary tissue death further compromises organ function and sometimes results in death of the individual. In addition, the resulting scar tissue that often forms can interfere with normal tissue function as occurs, for example, in idiopathic pulmonary fibrosis, IBD and organ cirrhosis.

[0046] The vascular endothelium constitutes the first barrier between circulating immune effector cells and extravascular tissues. Extravasation of these circulating cells requires that they bind to the vascular endothelial cells, cross the basement membrane, and enter insulted tissues e.g., by phagocytosis or protease-mediated extracellular matrix degradation. Without being limited to a particular theory, it is believed that the morphogens of this invention may modulate the inflammatory response in part by modulating the attachment of immune effector cells to the luminal side of the endothelium of blood vessels at or near sites of tissue damage and/or inflammatory lesions. Because the method reduces or prevents the attachment of immune effector cells at these sites, it also prevents the subsequent release of tissue destructive agents by these same immune effector cells at sites of tissue damage and/or inflammatory lesions. Because attachment of immune effector cells to the endothelium must precede their extravasation, the method also prevents the initial or continued entry of these cells into extravascular sites of tissue destruction or ongoing inflammatory lesions. Therefore, the invention not only relates to a method to reduce or prevent the immune cell-mediated cellular destruction at extravascular sites of recent tissue destruction, but also relates to a method to prevent or reduce the continued entry of immune effector cells into extravascular sites of ongoing inflammatory cascades. As will be appreciated by those skilled in the art, the morphogens of this invention also may be contemplated in mechanisms for disrupting the functional interaction of immune effector cells with endothelium where the adhesion molecules are induced by means other than in response to tissue injury.

[0047] One source of tissue injury is induced by cell exposure to toxic oxygen concentrations, such as ischemic-reperfusion tissue injury (oxygen deprivation), and following hyperoxia injury (lethally high oxygen concentrations). Accordingly, the process of the present invention provides a method for alleviating the tissue damage induced by ischemic-reperfusion injury or hyperoxia-induced injury comprising the step of administering to the afflicted individual a therapeutic amount of a morphogen prior to, during, or after damage to the affected tissue. Where the toxic oxygen concentrations may be deliberately induced, as by a surgical or clinical procedure, the morphogen preferably is administered prior to induction.

[0048] In addition, the morphogens described herein, in contrast to fibrogenic growth factors such as TGF- β , stimulate tissue morphogenesis and do not stimulate fibrosis or scar tissue formation (see Example 9, below.) Accordingly, in addition to inhibiting the tissue destructive effects associated with the inflammatory response, the morphogens further enhance the viability of damaged tissue and/or organs by stimulating the regeneration of the damaged tissue and preventing fibrogenesis.

[0049] The morphogens described herein also can inhibit epithelial cell proliferation (see Example 10, below.) This activity of the morphogens also may be particularly useful in the treatment of psoriasis and other inflammatory diseases that involve epithelial cell populations.

[0050] Provided below are detailed descriptions of suitable morphogens useful in the methods and compositions of this invention, as well as methods for their administration and application, and numerous, nonlimiting examples which 1) illustrate the suitability of the morphogens and morphogen-stimulating agents described herein as therapeutic agents for protecting tissue from the tissue destructive effects associated with the body's inflammatory response; and 2) provide assays with which to test candidate morphogens and morphogen-stimulating agents for their efficacy.

50 I. Useful Morphogens

[0051] As defined herein a protein is morphogenic if it is capable of inducing the developmental cascade of cellular and molecular events that culminate in the formation of new, organ-specific tissue and comprises at least the conserved C-terminal six cysteine skeleton or its functional equivalent (see supra). Specifically, the morphogens generally are capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells.

Details of how the morphogens useful in the method of this invention first were identified, as well as a description on how to make, use and test them for morphogenic activity are disclosed in USSN 667,274, filed March 11, 1991 and USSN 752,764, filed August 30, 1991. As disclosed therein, the morphogens may be purified from naturally-sourced material or recombinantly produced from procarcyotic or eucaryotic host cells, using the genetic sequences disclosed therein. Alternatively, novel morphogenic sequences may be identified following the procedures disclosed therein.

[0052] Particularly useful proteins include those which comprise the naturally derived sequences disclosed in Table II. Other useful sequences include biosynthetic constructs such as those disclosed in U.S. Pat. 5,011,691 (e.g., COP-1, COP-3, COP-4, COP-5, COP-7, and COP-16).

[0053] Accordingly, the morphogens useful in the methods and compositions of this invention also may be described by morphogenically active proteins having amino acid sequences sharing 70% or, preferably, 80% homology (similarity) with any of the sequences described above, where "homology" is as defined herein above.

[0054] The morphogens useful in the method of this invention also can be described by any of the 6 generic sequences described herein (Generic Sequences 1, 2, 3, 4, 5 and 6). Generic sequences 1 and 2 also may include, at their N-terminus, the sequence

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Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)

1 5

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[0055] Table II, set forth below, compares the amino acid sequences of the active regions of native proteins that have been identified as morphogens, including human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-23), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), BMP3 (Seq. ID No. 26), DPP (from *Drosophila*, Seq. ID No. 11), Vgl, (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), GDF-1 (from mouse, Seq. ID Nos. 14, 32 and 33), 60A protein (from *Drosophila*, Seq. ID Nos. 24 and 25), BMP5 (Seq. ID No. 27) and BMP6 (Seq. ID No. 28). The sequences are aligned essentially following the method of Needleman et al. (1970) *J. Mol. Biol.*, 48:443-453, calculated using the Align Program (DNAstar, Inc.). In the table, three dots indicates that the amino acid in that position is the same as the amino acid in hOP-1. Three dashes indicates that no amino acid is present in that position, and are included for purposes of illustrating homologies. For example, amino acid residue 60 of CBMP-2A and CBMP-2B is "missing". Of course, both these amino acid sequences in this region comprise Asn-Ser (residues 58, 59), with CBMP-2A then comprising Lys and Ile, whereas CBMP-2B comprises Ser and Ile.

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TABLE II

5	hOP-1	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
	mOP-1
	hOP-2	...	Arg	Arg
10	mOP-2	...	Arg	Arg
	DPP	...	Arg	Arg	...	Ser
	Vgl	Lys	Arg	His
15	Vgr-1	Gly
	CBMP-2A	Arg	...	Pro
	CBMP-2B	...	Arg	Arg	...	Ser
	BMP3	...	Ala	Arg	Arg	Tyr	...	Lys	...
20	GDF-1	...	Arg	Ala	Arg	Arg
	60A	...	Gln	Met	Glu	Thr
	BMP5
25	BMP6	...	Arg
		1				5			

30	hOP-1	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
	mOP-1
	hOP-2	Gln	Leu	...
35	mOP-2	Ser	Leu	...
	DPP	Asp	...	Ser	...	Val	Asp	...
	Vgl	Glu	...	Lys	...	Val	Asn
	Vgr-1	Gln	...	Val
40	CBMP-2A	Asp	...	Ser	...	Val	Asn	...
	CBMP-2B	Asp	...	Ser	...	Val	Asn	...
	BMP3	Asp	...	Ala	...	Ile	Ser	Glu
45	GDF-1	Glu	Val	His	Arg
	60A	Asp	...	Lys	His	...
	BMP5
50	BMP6	Gln
		10					15			

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	hOP-1	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
5	mOP-1
	hOP-2	...	Val	Gln	Ser
	mOP-2	...	Val	Gln	Ser
	DPP	Val	Leu	Asp
10	Vgl	...	Val	Gln	Met
	Vgr-1	Lys
	CBMP-2A	Val	Pro	His
15	CBMP-2B	Val	Pro	Gln
	BMP3	Ser	...	Lys	Ser	Phe	Asp
	GDF-1	...	Val	Arg	...	Phe	Leu
	60A	Gly
20	BMP5
	BMP6	Lys
					20					25
25										
	hOP-1	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	mOP-1
30	hOP-2	Ser
	mOP-2
	DPP	His	...	Lys	...	Pro
35	Vgl	...	Asn	Tyr	Pro
	Vgr-1	...	Asn	Asp	Ser
	CBMP-2A	...	Phe	His	...	Glu	...	Pro
	CBMP-2B	...	Phe	His	...	Asp	...	Pro
40	BMP3	Ser	...	Ala	...	Gln
	GDF-1	...	Asn	Gln	...	Gln
	60A	...	Phe	Ser	Asn
45	BMP5	...	Phe	Asp	Ser
	BMP6	...	Asn	Asp	Ser
					30					35
50	hOP-1	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
	mOP-1

	hOP-2	Asp	...	Cys
5	mOP-2	Asp	...	Cys
	DPP	Ala	Asp	His	Phe	...	Ser
	Vgl	Tyr	Thr	Glu	Ile	Leu	...	Gly
	Vgr-1	Ala	His
10	CBMP-2A	Ala	Asp	His	Leu	...	Ser
	CBMP-2B	Ala	Asp	His	Leu	...	Ser
	GDF-1	Leu	...	Val	Ala	Leu	Ser	Gly	Ser**	...
15	BMP3	Met	Pro	Lys	Ser	Leu	Lys	Pro
	60A	Ala	His
	BMP5	Ala	His	Met
	BMP6	Ala	His	Met
20							40			
	hOP-1	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
25	mOP-1
	hOP-2	Leu	...	Ser	...
	mOP-2	Leu	...	Ser	...
	DPP	Val
30	Vgl	Ser	Leu
	Vgr-1
	CBMP-2A
35	CBMP-2B
	BMP3	Ser	Thr	Ile	...	Ser	Ile
	GDF-1	Leu	Val	Leu	Arg	Ala	...
40	60A
	BMP5
	BMP6
		45					50			
45										
	hOP-1	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
50	mOP-1	Asp
	hOP-2	...	His	Leu	Met	Lys	...	Asn	Ala	...
	mOP-2	...	His	Leu	Met	Lys	...	Asp	Val	...

	DPP	...	Asn	Asn	Asn	Gly	Lys	...
5	Vgl	Ser	...	Glu	Asp	Ile
	Vgr-1	Val	Met	Tyr	...
	CBMP-2A	...	Asn	Ser	Val	...	Ser	---	Lys	Ile
	CBMP-2B	...	Asn	Ser	Val	...	Ser	---	Ser	Ile
10	BMP3	...	Arg	Ala**	Gly	Val	Val	Pro	Gly	Ile
	GDF-1	Met	...	Ala	Ala	Ala	...	Gly	Ala	Ala
	60A	Leu	Leu	Glu	...	Lys	Lys	...
	BMP5	Leu	Met	Phe	...	Asp	His	...
15	BMP6	Leu	Met	Tyr	...
						55				60

20	hOP-1	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	mOP-1
	hOP-2	Ala	Lys
25	mOP-2	Ala	Lys
	DPP	Ala	Val
	Vgl	...	Leu	Val	Lys
30	Vgr-1	Lys
	CBMP-2A	Ala	Val	Glu
	CBMP-2B	Ala	Val	Glu
35	BMP3	...	Glu	Val	...	Glu	Lys
	GDF-1	Asp	Leu	Val	...	Ala	Arg
	60A	Arg
	BMP5	Lys
40	BMP6	Lys
						65				70

45	hOP-1	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	mOP-1
	hOP-2	...	Ser	...	Thr	Tyr
	mOP-2	...	Ser	...	Thr	Tyr
50	Vgl	Met	Ser	Pro	Met	...	Phe	Tyr
	Vgr-1	Val

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	DPP	...	Asp	Ser	Val	Ala	Met	Leu
5	CBMP-2A	...	Ser	Met	Leu
	CBMP-2B	...	Ser	Met	Leu
	BMP3	Met	Ser	Ser	Leu	...	Ile	...	Phe	Tyr
	GDF-1	...	Ser	Pro	Phe	...
10	60A	...	Gly	...	Leu	Pro	His
	BMP5
	BMP6
					75					80
15										
	hOP-1	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
	mOP-1
20	hOP-2	...	Ser	...	Asn	Arg
	mOP-2	...	Ser	...	Asn	Arg
	DPP	Asn	...	Gln	...	Thr	...	Val
25	Vgl	...	Asn	Asn	Asp	Val	...	Arg
	Vgr-1	Asn
	CBMP-2A	...	Glu	Asn	Glu	Lys	...	Val
	CBMP-2B	...	Glu	Tyr	Asp	Lys	...	Val
30	BMP3	...	Glu	Asn	Lys	Val
	GDF-1	...	Asn	...	Asp	Val	...	Arg
	60A	Leu	Asn	Asp	Glu	Asn
35	BMP5
	BMP6	Asn
					85					
40										
	hOP-1	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	
	mOP-1
45	hOP-2	...	His	Lys	
	mOP-2	...	His	Lys	
	DPP	Asn	...	Gln	Glu	...	Thr	...	Val	
50	Vgl	His	...	Glu	Ala	...	Asp	
	Vgr-1
	CBMP-2A	Asn	...	Gln	Asp	Glu	

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	CBMP-2B	Asn	...	Gln	Glu	Glu
5	BMP3	Val	...	Pro	Thr	Glu
	GDF-1	Gln	...	Glu	Asp	Asp
	60A	Ile	Lys
	BMP5
10	BMP6	Trp
			90				95			
15	hOP-1	Ala	Cys	Gly	Cys	His				
	mOP-1				
	hOP-2				
20	mOP-2				
	DPP	Gly	Arg				
	Vgl	Glu	Arg				
25	Vgr-1				
	CBMP-2A	Gly	Arg				
	CBMP-2B	Gly	Arg				
	BMP3	Ser	...	Ala	...	Arg				
30	GDF-1	Glu	Arg				
	60A	Ser				
	BMP5	Ser				
35	BMP6				
					100					

**Between residues 56 and 57 of BMP3 is a Val residue;
 between residues 43 and 44 of GDF-1 lies
 the amino acid sequence Gly-Gly-Pro-Pro.

45 [0056] As is apparent from the foregoing amino acid sequence comparisons, significant amino acid changes can be made within the generic sequences while retaining the morphogenic activity. For example, while the GDF-1 protein sequence depicted in Table II shares only about 50% amino acid identity with the hOP1 sequence described therein, the GDF-1 sequence shares greater than 70% amino acid sequence homology (or "similarity") with the hOP1 sequence, where "homology" or "similarity" includes allowed conservative amino acid changes within the sequence as defined by Dayoff, et al., Atlas of Protein Sequence and Structure vol.5, supp.3, pp.345-362, (M.O. Dayoff, ed., Nat'l BioMed. Res. Fd'n, Washington D.C. 1979.)

[0057] The currently most preferred protein sequences useful as morphogens in this invention include those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both 55 allelic and species variants of the OP-1 and OP-2 proteins, including the Drosophila 60A protein. Accordingly, in still another preferred aspect, the invention includes morphogens comprising species of polypeptide chains having the generic amino acid sequence referred to herein as "OPX", which defines the seven cysteine skeleton and accommodates the identities between the various identified mouse and human OP1 and OP2 proteins. OPX is presented in Seq.

ID No. 29. As described therein, each Xaa at a given position independently is selected from the residues occurring at the corresponding position in the C-terminal sequence of mouse or human OP1 or OP2 (see Seq. ID Nos. 5-8 and/or Seq. ID Nos. 16-23).

5 II. Formulations and Methods for Administering Therapeutic Agents

[0058] The morphogens may be provided to an individual by any suitable means, preferably directly (e.g., locally, as by injection or topical administration to a tissue locus) or systemically (e.g., parenterally or orally). Where the morphogen is to be provided parenterally, such as by intravenous, subcutaneous, intramuscular, intraorbital, ophthalmic, 10 intraventricular, intracranial, intracapsular, intraspinal, intracisternal, intraperitoneal, buccal, rectal, vaginal, intranasal or by aerosol administration, the morphogen preferably comprises part of an aqueous solution. The solution is physiologically acceptable so that in addition to delivery of the desired morphogen to the patient, the solution does not otherwise adversely affect the patient's electrolyte and volume balance. The aqueous medium for the morphogen thus may comprise normal physiologic saline (9.85% NaCl, 0.15M), pH 7-7.4. The aqueous solution containing the morphogen 15 can be made, for example, by dissolving the protein in 50% ethanol containing acetonitrile in 0.1% trifluoroacetic acid (TFA) or 0.1% HCl, or equivalent solvents. One volume of the resultant solution then is added, for example, to ten volumes of phosphate buffered saline (PBS), which further may include 0.1-0.2% human serum albumin (HSA). The resultant solution preferably is vortexed extensively. If desired, a given morphogen may be made more soluble by association with a suitable molecule. For example, association of the mature dimer with the pro domain of the morphogen 20 keeps the morphogen soluble in physiological buffers. In fact, the endogenous protein is thought to be transported in this form. Another molecule capable of enhancing solubility and particularly useful for oral administrations, is casein. For example, addition of 0.2% casein increases solubility of the mature active form of OP-1 by 80%. Other components found in milk and/or various serum proteins also may be useful.

[0059] Useful solutions for parenteral administration may be prepared by any of the methods well known in the pharmaceutical art, described, for example, in *Remington's Pharmaceutical Sciences* (Gennaro, A., ed.), Mack Pub., 25 1990. Formulations may include, for example, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, hydrogenated naphthalenes, and the like. Formulations for direct administration, in particular, may include glycerol and other compositions of high viscosity to help maintain the morphogen at the desired locus. Biocompatible, preferably bioresorbable, polymers, including, for example, hyaluronic acid, collagen, tricalcium phosphate, polybutyrate, lactide 30 and glycolide polymers, and lactide/glycolide copolymers, may be useful excipients to control the release of the morphogen *in vivo*. Other potentially useful parenteral delivery systems for these morphogens include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation administration contain as excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or oily solutions for administration in the form of nasal drops, or as 35 a gel to be applied intranasally. Formulations for parenteral administration may also include glycocholate for buccal administration, methoxysalicylate for rectal administration, or cutric acid for vaginal administration.

[0060] Suppositories for rectal administration also may be prepared by mixing the morphogen or morphogen-stimulating agent with a non-irritating excipient such as cocoa butter or other compositions which are solid at room temperature and liquid at body temperatures.

[0061] Formulations for topical administration to the skin surface may be prepared by dispersing the morphogen or morphogen-stimulating agent with a dermally acceptable carrier such as a lotion, cream, ointment or soap. Particularly useful are carriers capable of forming a film or layer over the skin to localize application and inhibit removal. For topical administration to internal tissue surfaces, the morphogen may be dispersed in a liquid tissue adhesive or other substance known to enhance adsorption to a tissue surface. For example, hydroxypropylcellulose or fibrinogen/thrombin 40 45 solutions may be used to advantage. Alternatively, tissue-coating solutions, such as pectin-containing formulations, may be used.

[0062] Alternatively, the morphogens described herein may be administered orally. Oral administration of proteins as therapeutics generally is not practiced as most proteins are readily degraded by digestive enzymes and acids in the mammalian digestive system before they can be absorbed into the bloodstream. However, the morphogens described 50 55 herein typically are acid stable and protease-resistant (see, for example, U.S. Pat.No. 4,968,590.) In addition, at least one morphogen, OP-1, has been identified in mammary gland extract, colostrum and 57-day milk. Moreover, the OP-1 purified from mammary gland extract is morphogenically active. Specifically, this protein induces endochondral bone formation in mammals when implanted subcutaneously in association with a suitable matrix material, using a standard *in vivo* bone assay, such as is disclosed in U.S. Pat.No. 4,968,590. Moreover, the morphogen also is detected in the bloodstream. Finally, soluble form morphogen, e.g., mature morphogen associated with the pro domain, is morphogenically active. These findings indicate that oral and parenteral administration are viable means for administering morphogens to an individual. In addition, while the mature forms of certain morphogens described herein typically are sparingly soluble, the morphogen form found in milk (and mammary gland extract and colostrum) is readily soluble,

probably by association of the mature, morphogenically active form with part or all of the pro domain of the intact sequence and/or by association with one or more milk components. Accordingly, the compounds provided herein also may be associated with molecules capable of enhancing their solubility *in vitro* or *in vivo*.

[0063] Where the morphogen or morphogen-stimulating agent comprises part of a tissue or organ preservation solution, any commercially available preservation solution may be used to advantage. For example, useful solutions known in the art include Collins solution, Wisconsin solution, Belzer solution, Eurocollins solution and lactated Ringer's solution. Generally, an organ preservation solution usually possesses one or more of the following properties: (a) an osmotic pressure substantially equal to that of the inside of a mammalian cell,(solutions typically are hyperosmolar and have K⁺ and/or Mg⁺⁺ ions present in an amount sufficient to produce an osmotic pressure slightly higher than the inside of a mammalian cell; (b) the solution typically is capable of maintaining substantially normal ATP levels in the cells; and (c) the solution usually allows optimum maintenance of glucose metabolism in the cells. Organ preservation solutions also may contain anticoagulants, energy sources such as glucose, fructose and other sugars, metabolites, heavy metal chelators, glycerol and other materials of high viscosity to enhance survival at low temperatures, free oxygen radical inhibiting agents and a pH indicator. A detailed description of preservation solutions and useful components may be found, for example, in US Patent No. 5,002,965.

[0064] The compounds provided herein also may be associated with molecules capable of targeting the morphogen or morphogen-stimulating agent to the desired tissue. For example, an antibody, antibody fragment, or other binding protein that interacts specifically with a surface molecule on cells of the desired tissue, may be used. Useful targeting molecules may be designed, for example, using the single chain binding site technology disclosed, for example, in U.S. Pat. No. 5,091,513.

[0065] As described above, the morphogens provided herein share significant sequence homology in the C-terminal active domains. By contrast, the sequences typically diverge significantly in the sequences which define the pro domain. Accordingly, the pro domain is thought to be morphogen-specific. As described above, it is also known that the various morphogens identified to date are differentially expressed in the different tissues. Accordingly, without being limited to any given theory, it is likely that, under natural conditions in the body, selected morphogens typically act on a given tissue. Accordingly, part or all of the pro domains which have been identified associated with the active form of the morphogen in solution, may serve as targeting molecules for the morphogens described herein. For example, the pro domains may interact specifically with one or more molecules at the target tissue to direct the morphogen associated with the pro domain to that tissue. Accordingly, another useful targeting molecule for targeting morphogen to a tissue of interest is part or all of a morphogen pro domain. For example, part or all of the pro domain of GDF-1 may be used to target a morphogen to nerve tissue. Alternatively, part or all of the pro domain of OP-1 or CBMP2 may be used to target a morphogen to bone tissue, both of which proteins are found naturally associated with bone tissue.

[0066] The morphogens described herein are useful for providing neuroprotective effects to alleviate neural pathway damage associated with the body's immune/inflammatory response to an initial injury to nerve tissue. As used herein, a "neural pathway" describes a nerve circuit for the passage of electric signals from a source to a target cell site and includes both the central nervous system (CNS) and peripheral nervous system (PNS). The pathway includes the neurons through which the electric impulse is transported, including groups of interconnecting neurons, the nerve fibers formed by bundled neuronal axons, and the glial cells surrounding and associated with the neurons. An inflammatory response to nerve tissue injury may follow trauma to nerve tissue, caused, for example, by an autoimmune (including autoantibody) dysfunction, neoplastic lesion, infection, chemical or mechanical trauma, or other disease. An exemplary nerve-related inflammatory disease is multiple sclerosis. Neural pathway damage also can result from a reduction or interruption, e.g., occlusion, of a neural blood supply, as in an embolic stroke, (e.g, ischemia or hypoxia-induced injury), or by other trauma to the nerve or surrounding material. In addition, at least part of the damage associated with a number of primary brain tumors also appears to be immunologically related. Application of the morphogen directly to the cells to be treated, or providing the morphogen to the mammal systemically, for example, intravenously or indirectly by oral administration, may be used to alleviate and/or inhibit the immunologically related response to a neural injury. Alternatively, administration of an agent capable of stimulating morphogen expression and/or secretion *in vivo*, preferably at the site of injury, also may be used. Where the injury is to be induced, as during surgery or other aggressive clinical treatment, the morphogen or agent may be provided prior to induction of the injury to provide a neuroprotective effect to the nerve tissue at risk.

[0067] Where the morphogen is intended for use as a therapeutic to alleviate tissue damage associated with an immune/inflammatory condition of the CNS, an additional problem must be addressed: overcoming the so-called "blood-brain barrier", the brain capillary wall structure that effectively screens out all but selected categories of molecules present in the blood, preventing their passage into the brain. The blood-brain barrier may be bypassed effectively by direct infusion of the morphogen or morphogen-stimulating agent into the brain. Alternatively, the morphogen or morphogen-stimulating agent may be modified to enhance its transport across the blood-brain barrier. For example, truncated forms of the morphogen or a morphogen-stimulating agent may be most successful. Alternatively, the morphogen or morphogen-stimulating agent may be modified to render it more lipophilic, or it may be conjugated to another mole-

cule which is naturally transported across the barrier, using standard means known to those skilled in the art, as, for example, described in Pardridge, *Endocrine Reviews* 7:314-330 (1986) and U.S. Pat. No. 4,801,575.

[0068] Finally, the morphogens or morphogen-stimulating agents provided herein may be administered alone or in combination with other molecules known to be beneficial in the treatment compositions and methods described herein, including, but not limited to anticoagulants, free oxygen radical inhibiting agents, salicylic acid, vitamin D, and other anti-inflammatory agents. Psoriasis treatments also may include ultra-violet light treatment, zinc oxide and retinoids.

[0069] The compounds provided herein can be formulated into pharmaceutical compositions by admixture with pharmaceutically acceptable nontoxic excipients and carriers. As noted above, such compositions may be prepared for parenteral administration, particularly in the form of liquid solutions or suspensions; for oral administration, particularly in the form of tablets or capsules; or intranasally, particularly in the form of powders, nasal drops, or aerosols.

[0070] The compositions can be formulated for parenteral or oral administration to humans or other mammals in therapeutically effective amounts, e.g., amounts which provide appropriate concentrations for a time sufficient to alleviate the tissue destructive effects associated with the inflammatory response, including protecting tissue in anticipation of tissue damage.

[0071] As will be appreciated by those skilled in the art, the concentration of the compounds described in a therapeutic composition will vary depending upon a number of factors, including the dosage of the drug to be administered, the chemical characteristics (e.g., hydrophobicity) of the compounds employed, and the route of administration. The preferred dosage of drug to be administered also is likely to depend on such variables as the type and extent of progression of the tissue damage, the overall health status of the particular patient, the relative biological efficacy of the compound selected, the formulation of the compound excipients, and its route of administration. In general terms, the compounds of this invention may be provided in an aqueous physiological buffer solution containing about 0.001% to 10% w/v compound for parenteral administration. Typical dose ranges are from about 10 ng/kg to about 1 g/kg of body weight per day; a preferred dose range is from about 0.1 µg/kg to 100 mg/kg of body weight per day. Optimally, the morphogen dosage given is between 0.1-100 µg of protein per kilogram weight of the patient. No obvious morphogen induced pathological lesions are induced when mature morphogen (e.g., OP-1, 20 µg) is administered daily to normal growing rats for 21 consecutive days. Moreover, 10 µg systemic injections of morphogen (e.g., OP-1) injected daily for 10 days into normal newborn mice does not produce any gross abnormalities.

[0072] In administering morphogens systemically in the methods of the present invention, preferably a large volume loading dose is used at the start of the treatment. The treatment then is continued with a maintenance dose. Further administration then can be determined by monitoring at intervals the levels of the morphogen in the blood.

[0073] Where tissue injury is induced deliberately as part of, for example, a surgical procedure, the morphogen preferably is provided just prior to, or concomitant with induction of the trauma. Preferably, the morphogen is administered prophylactically in a surgical setting.

[0074] Alternatively, an effective amount of an agent capable of stimulating endogenous morphogen levels may be administered by any of the routes described above. For example, an agent capable of stimulating morphogen production and/or secretion from cells of affected tissue and/or transplant tissue may be provided to a mammal, e.g., by direct administration of the agent to the tissue to be treated. A method for identifying and testing agents capable of modulating the levels of endogenous morphogens in a given tissue is described generally herein in Example 15, and in detail in copending USSN 752,859, filed August 30, 1991. Briefly, candidate compounds can be identified and tested by incubating the compound *in vitro* with a test tissue or cells thereof, for a time sufficient to allow the compound to affect the production, i.e., the expression and/or secretion, of a morphogen produced by the cells of that tissue.

[0075] For purposes of the present invention, the above-described morphogens effective in alleviating tissue damage associated with ischemic-reperfusion injury (or the agents that stimulate them, referred to collectively herein as "therapeutic agent") are administered prior to or during the restoration of oxygen (e.g., restoration of blood flow, reperfusion.) Where treatment is to follow an existing injury, the therapeutic agent preferably is administered as an intravenous infusion provided acutely after the hypoxic or ischemic condition occurs. For example, the therapeutic agent can be administered by intravenous infusion immediately after a cerebral infarction, a myocardial infarction, asphyxia, or a cardiopulmonary arrest. Where ischemia or hypoxia injury is deliberately and/or unavoidably induced as part of, for example, a surgical procedure where circulation to an organ or organ system is deliberately and/or transiently interrupted, e.g., in carotid enterectomy, coronary artery bypass, grafting, organ transplanting, fibrinolytic therapy, etc., the therapeutic agent preferably is provided just prior to, or concomitant with, reduction of oxygen to the tissue. Preferably, the morphogen is administered prophylactically in a surgical setting.

[0076] Similarly, where hyperoxia-induced injury already has occurred, the morphogen is administered upon diagnosis. Where hyperoxia injury may be induced as, for example, during treatment of prematurely newborn babies, or patients suffering from pulmonary diseases such as emphysema, the therapeutic agent preferably is administered prior to administration of oxygen e.g., prophylactically.

III. Examples**Example 1. Identification of Morphogen-Expressing Tissue**

5 [0077] Determining the tissue distribution of morphogens may be used to identify different morphogens expressed in a given tissue, as well as to identify new, related morphogens. Tissue distribution also may be used to identify useful morphogen-producing tissue for use in screening and identifying candidate morphogen-stimulating agents. The morphogens (or their mRNA transcripts) readily are identified in different tissues using standard methodologies and minor modifications thereof in tissues where expression may be low. For example, protein distribution may be determined
 10 using standard Western blot analysis or immunofluorescent techniques, and antibodies specific to the morphogen or morphogens of interest. Similarly, the distribution of morphogen transcripts may be determined using standard Northern hybridization protocols and transcript-specific probes.

[0078] Any probe capable of hybridizing specifically to a transcript, and distinguishing the transcript of interest from other, related transcripts may be used. Because the morphogens described herein share such high sequence homology in their active, C-terminal domains, the tissue distribution of a specific morphogen transcript may best be determined using a probe specific for the pro region of the immature protein and/or the N-terminal region of the mature protein. Another useful sequence is the 3' non-coding region flanking and immediately following the stop codon. These portions of the sequence vary substantially among the morphogens of this invention, and accordingly, are specific for each protein. For example, a particularly useful Vgr-1-specific probe sequence is the Pvull-Sacl fragment, a 265 bp
 20 fragment encoding both a portion of the untranslated pro region and the N-terminus of the mature sequence (see Lyons et al. (1989) *PNAS* 86:4554-4558 for a description of the cDNA sequence). Similarly, particularly useful mOP-1-specific probe sequences are the BstX1-BgII fragment, a 0.68 Kb sequence that covers approximately two-thirds of the mOP-1 pro region; a Stu1-Stu1 fragment, a 0.2 Kb sequence immediately upstream of the 7-cysteine domain; and the Ear1-Pst1 fragment, an 0.3 Kb fragment containing a portion of the 3'untranslated sequence (See Seq. ID No. 18, where the pro region is defined essentially by residues 30-291.) Similar approaches may be used, for example, with hOP-1 (Seq. ID No. 16) or human or mouse OP-2 (Seq. ID Nos. 20 and 22.)

[0079] Using these morphogen-specific probes, which may be synthetically engineered or obtained from cloned sequences, morphogen transcripts can be identified in mammalian tissue, using standard methodologies well known to those having ordinary skill in the art. Briefly, total RNA is prepared from various adult murine tissues (e.g., liver, kidney, testis, heart, brain, thymus and stomach) by a standard methodology such as by the method of Chomczyaski et al.
 30 ((1987) *Anal. Biochem.* 162:156-159) and described below. Poly (A)+ RNA is prepared by using oligo (dT)-cellulose chromatography (e.g., Type 7, from Pharmacia LKB Biotechnology, Inc.). Poly (A)+ RNA (generally 15 µg) from each tissue is fractionated on a 1% agarose/formaldehyde gel and transferred onto a Nytran membrane (Schleicher & Schuell). Following the transfer, the membrane is baked at 80°C and the RNA is cross-linked under UV light (generally
 35 30 seconds at 1 mW/cm²). Prior to hybridization, the appropriate probe is denatured by heating. The hybridization is carried out in a lucite cylinder rotating in a roller bottle apparatus at approximately 1 rev/min for approximately 15 hours at 37°C using a hybridization mix of 40% formamide, 5 x Denhardt's, 5 x SSPE, and 0.1% SDS. Following hybridization, the non-specific counts are washed off the filters in 0.1 x SSPE, 0.1% SDS at 50°C.

[0080] Examples demonstrating the tissue distribution of various morphogens, including Vgr-1, OP-1, BMP2,
 40 BMP3, BMP4, BMP5, GDF-1, and OP-2 in developing and adult tissue are disclosed in co-pending USSN 752,764, and in Ozkaynak, et al., (1991) *Biochem. Biophys. Res. Commun.* 179:116-123, and Ozkaynak, et al. (1992) (JBC, in press). Using the general probing methodology described herein, northern blot hybridizations using probes specific for these morphogens to probe brain, spleen, lung, heart, liver and kidney tissue indicate that kidney-related tissue appears to be the primary expression source for OP-1, with brain, heart and lung tissues being secondary sources. OP-1 mRNA
 45 also was identified in salivary glands, specifically rat parotid glands, using this probing methodology. Lung tissue appears to be the primary tissue expression source for Vgr-1, BMP5, BMP4 and BMP3. Lower levels of Vgr-1 also are seen in kidney and heart tissue, while the liver appears to be a secondary expression source for BMP5, and the spleen appears to be a secondary expression source for BMP4. GDF-1 appears to be expressed primarily in brain tissue. To date, OP-2 appears to be expressed primarily in early embryonic tissue. Specifically, northern blots of murine embryos
 50 and 6-day post-natal animals shows abundant OP2 expression in 8-day embryos. Expression is reduced significantly in 17-day embryos and is not detected in post-natal animals.

Example 2. Active Morphogens in Body Fluids

55 [0081] OP-1 expression has been identified in saliva (specifically, the rat parotid gland, see Example 1), human blood serum, and various milk forms, including mammary gland extract, colostrum, and 57-day bovine milk. Moreover, and as described in USSN 923,780, the body fluid-extracted protein is morphogenically active. The discovery that the morphogen naturally is present in milk and saliva, together with the known observation that mature, active OP-1 is acid-

stable and protease-resistant, indicate that oral administration is a useful route for therapeutic administration of morphogen to a mammal. Oral administration typically is the preferred mode of delivery for extended or prophylactic therapies. In addition, the identification of morphogen in all milk forms, including colostrum, suggests that the protein may play a significant role in tissue development, including skeletal development, of juveniles.

5

2.1 Morphogen Detection in Milk

[0082] OP-1 was partially purified from rat mammary gland extract and bovine colostrum and 57 day milk by passing these fluids over a series of chromatography columns: (e.g., cation-exchange, affinity and reverse phase). At each 10 step the eluant was collected in fractions and these were tested for the presence of OP-1 by standard immunoblot. Immunoreactive fractions then were combined and purified further. The final, partially purified product then was examined for the presence of OP-1 by Western blot analysis using OP-1-specific antisera, and tested for *in vivo* and *in vitro* activity.

[0083] OP-1 purified from the different milk sources were characterized by Western blotting using antibodies raised 15 against OP-1 and BMP2. Antibodies were prepared using standard immunology protocols well known in the art, and as described generally in Example 15, below, using full-length *E. coli*-produced OP-1 and BMP2 as the immunogens. In all cases, the purified OP-1 reacted only with the anti-OP-1 antibody, and not with anti-BMP2 antibody.

[0084] The morphogenic activity of OP-1 purified from mammary gland extract was evaluated *in vivo* essentially following the rat model assay described in U.S. Pat. No. 4,968,590. Briefly, a sample was prepared from each OP-1 immunoreactive fraction of the mammary gland extract-derived OP-1 final product by lyophilizing a portion (33%) of the 20 fraction and resuspending the protein in 220 μ l of 50% acetonitrile/0.1% TFA. After vortexing, 25 mg of collagen matrix was added. The samples were lyophilized overnight, and implanted in Long Evans rats (Charles River Laboratories, Wilmington, MA, 28-35 days old). Each fraction was implanted in duplicate. For details of the collagen matrix implantation procedure, see, for example, U.S. Pat. No. 4,968,590. After 12 days, the implants were removed and evaluated for 25 new bone formation by histological observation as described in U.S. Patent No. 4,968,590. In all cases, the immunoreactive fractions were osteogenically active.

2.2 Morphogen Detection in Serum

[0085] Morphogen may be detected in serum using morphogen-specific antibodies. The assay may be performed 30 using any standard immunoassay, such as Western blot (immunoblot) and the like. Preferably, the assay is performed using an affinity column to which the morphogen-specific antibody is bound and through which the sample serum then is poured, to selectively extract the morphogen of interest. The morphogen then is eluted. A suitable elution buffer may be determined empirically by determining appropriate binding and elution conditions first with a control (e.g., purified, 35 recombinantly-produced morphogen.) Fractions then are tested for the presence of the morphogen by standard immunoblot, and the results confirmed by N-terminal sequencing. Preferably, the affinity column is prepared using monoclonal antibodies. Morphogen concentrations in serum or other fluid samples then may be determined using standard protein quantification techniques, including by spectrophotometric absorbance or by quantitation of conjugated antibody.

[0086] Presented below is a sample protocol for identifying OP-1 in serum. Following this general methodology 40 other morphogens may be detected in body fluids, including serum. The identification of morphogen in serum further indicates that systemic administration is a suitable means for providing therapeutic concentrations of a morphogen to an individual, and that morphogens likely behave systemically as endocrine-like factors. Finally, using this protocol, fluctuations in endogenous morphogen levels can be detected, and these altered levels may be used as an indicator of tissue dysfunction. Alternatively, fluctuations in morphogen levels may be assessed by monitoring morphogen 45 transcription levels, either by standard northern blot analysis as described in Example 1, or by *in situ* hybridization, using a labelled probe capable of hybridizing specifically to morphogen mRNA, and standard RNA hybridization protocols well described in the art and described generally in Example 1.

[0087] OP-1 was detected in human serum using the following assay. A monoclonal antibody raised against mammalian, recombinantly produced OP-1 using standard immunology techniques well described in the art and described 50 generally in Example 15, was immobilized by passing the antibody over an agarose-activated gel (e.g., Affi-Gel™, from Bio-Rad Laboratories, Richmond, CA, prepared following manufacturer's instructions) and used to purify OP-1 from serum. Human serum then was passed over the column and eluted with 3M K-thiocyanate. K-thiocyanate fractions then were dialyzed in 6M urea, 20mM PO₄, pH 7.0, applied to a C8 HPLC column, and eluted with a 20 minute, 25-50% 55 acetonitrile/0.1% TFA gradient. Mature, recombinantly produced OP-1 homodimers elute between 20-22 minutes. Fractions then were collected and tested for the presence of OP-1 by standard immunoblot using an OP-1 specific antibody as for Example 2.A.

[0088] Administered or endogenous morphogen levels may be monitored in the therapies described herein by com-

paring the quantity of morphogen present in a body fluid sample with a predetermined reference value, for example, to evaluate the efficiency of a therapeutic protocol, and the like. In addition, fluctuations in the level of endogenous morphogen antibodies may be detected by this method, most likely in serum, using an antibody or other binding protein capable of interacting specifically with the endogenous morphogen antibody. Detected fluctuations in the levels of the morphogen or endogenous antibody may be used, for example, as indicators of a change in tissue status. For example, as damaged tissue is regenerated and the tissue or organ's function returns to "normal" and, in the absence of additional tissue damage, lower doses of morphogen may be required, and a higher level of circulating morphogen antibody may be measured.

10 Example 3. Effect of Morphogen after the Onset of the Ischemic Process

[0089] The cardioprotective effect of morphogens following ischemic-reperfusion injury in a mammal can readily be assessed in a rat model. In this example, morphogen (e.g., OP-1) is administered just prior to the onset of the ischemic process in experimentally-induced myocardial infarcted rats, essentially following the method of Lefer, et al. (1990) *Science* 249:61-64 and (1992) *J. Mol. Cell. Cardiol.* 24: 385-393. Briefly, loss of myocardial tissue function following ischemia and reperfusion is assayed by measuring loss of myocardial creatine kinase activity (CK) and loss of endothelium-dependent vasorelaxation function (see Example 4, below).

[0090] In a first group of ether-anesthetized rats, the left coronary artery was occluded just proximal to the first main branch with a silk ligature to induce a myocardial infarction (MI). The ligature was removed 10 minutes after occlusion 20 to allow for coronary reperfusion. This first group is referred to herein as the "myocardial infarcted" (MI) group. A second group of rats underwent the same procedure except that the coronary artery was not occluded, and thus no myocardial infarction occurred. The second group of rats is referred to herein as the "sham myocardial infarcted group" (SHAM MI).

[0091] The first group of rats, the MI group of rats, further was divided into three sub-groups. 2 μ g of morphogen (OP-1) were injected intravenously into the first sub-group of MI rats 10 minutes after ligation, immediately before reperfusion; into the second sub-group of MI rats 20 μ g of OP-1 were injected intravenously 10 minutes after ligation and 25 immediately before reperfusion; and into the third sub-group of MI rats (control) was injected vehicle only, e.g., 0.9% NaCl, as for the OP-1 treated rats.

[0092] Twenty-four hours later, the hearts were removed from all of the rats and the levels of creatine kinase (CK) from the left ventricle (the infarcted region) and from the interventricular septum (the control nonischemic region) were 30 determined by standard means. By comparing the difference in CK activities in both regions, the amount of CK activity lost from the infarcted region was used as an index of cardiac cellular injury to the infarcted region.

[0093] As shown in Figure 1, the data indicate that morphogens (e.g., OP-1) can provide significant cardioprotective effect when provided to ischemic tissue. In the figure, CK loss is graphed as the difference in specific CK activity between the interventricular septum and the left ventricle.

[0094] The loss of CK activity by the subgroup of MI rats which received 2 μ g of OP-1 just before reperfusion 35 showed some protection as compared with the control MI rats which received injections of vehicle alone, when the levels from both subgroups are measured against, and compared to, the levels obtained for the SHAM MI control. Significant cardioprotection was observed in the subgroup of MI rats which received 20 μ g of OP-1 immediately before reperfusion as compared with the control MI rats which received injections of vehicle alone, when the levels from both 40 subgroups are measured against, and compared to, the levels contained within the SHAM MI control.

[0095] These data indicate that OP-1 offers significant cardiac protection when administered after ischemia and before reperfusion.

[0096] A variation of this example also may be performed providing morphogen to the animal prior to induction of 45 ischemia. The experiments may be performed both in normal and immune-compromised rats to assess the cardioprotective effects of morphogen administered prior to ischemia.

Example 4. Vasodilation of Myocardial Infarcted Cardiac Tissue Treated with Morphogen

[0097] Certain vasodilators like acetylcholine (ACh) and adenosine diphosphate (ADP, an immune mediator) exert 50 their vasodilation activity only in the presence of intact endothelium, which is stimulated to release a substance termed endothelium-derived relaxing factor (EDRF). If the endothelium is injured so that EDRF is not released, no vasodilation occurs in response to these endothelium-dependent agents. In contrast, several other vasodilators including nitroglycerine (NTG) and nitroprusside, are endothelium-independent dilators, as they dilate blood vessels directly.

[0098] The present example demonstrates the ability of OP-1 to prevent the loss of cardioendothelium-dependent 55 relaxation (EDR) activity in the coronary microvasculature following reperfusion of ischemic myocardium, and their ability to reduce myocardial injury 24 hours after morphogen treatment. Briefly, 2 or 24 hours after morphogen treatment ischemia-reperfusion injury is induced in isolated rat hearts, the reperfused hearts are are vasodilated with either ACh or NTG. In the absence of morphogen treatment, injured tissue should inhibit ACh-induced vasodilation, but not NTG-

induced vasodilation. Morphogen treatment is expected to enhance ACh-induced vasodilation in the reperfused hearts.

[0099] Accordingly, 48 adult male Sprague-Dawley rats (250-330 g) were divided into eight groups of 6 rats each. Twelve rats were subjected to sham myocardial infarcts (SHAM MI) as described in Example 3. The hearts of the remaining 36 rats were isolated as follows: one set of twelve rats was injected intravenously with OP-1 24 hours prior to isolation of the heart; another set of rats was injected intravenously with 20 μ g of OP-1 2 hours prior to isolation of the heart; the final group of rats was injected with vehicle only (e.g., 0.9% NaCl.). The rats then were anesthetized with pentobarbital sodium (35 mg/kg, intraperitoneal); their hearts were isolated and perfused by the Langendorff method at a constant flow (15 ml/min) with oxygenated Krebs-Henseleit solution (Aoki et al. (1988) *J. Pharmacol.* **95**:35).

[0100] Each group of rats then were divided into two subgroups of six rats each. Twenty minutes before reperfusion, coronary vasodilator response was measured by inducing constriction with 0.05 μ mol U-44619 (9,11-methanepoxy-prostaglandin H₂) followed by a vasodilating agent 3 minutes later: subgroup one - 15 nmol ACh; subgroup 2 - 15 nmol NTG and the increase in coronary perfusion pressure (CPP) level measured as an indication of vasodilation. When CPP levels returned to normal, the hearts were subjected to ischemia by reducing coronary infusion to 15% of control flow for 30 minutes, then reestablishing normal flow, i.e., reperfusion, for an additional 20 minutes.

[0101] The vasodilator response then was remeasured by constriction and administration of vasodilating agent as described above.

[0102] The results of these experiments are shown in FIG 2. Before the ischemic event, both Ach and NTG gave normal vasorelaxant results in all events. The hearts which received OP-1 24 hours prior to ischemia showed an approximately 70% response to ACh while the hearts which received OP-1 2 hours prior to ischemia showed a 55% response to ACh. The group which received vehicle alone showed a 40% response to ACh. Finally, the control group which was not subjected to ischemia showed an ACh response of approximately 95%. This shows that endothelium-dependent vasodilators exert a reduced vasodilator response following ischemia and reperfusion in the rat heart. Moreover, OP-1 significantly preserved endothelium-dependent dilation when provided 24 hours prior to induction of myocardial ischemia. No defect in vasodilation occurred in response to the direct vasodilator (NTG); NTG-induced vasodilation activities were 95% of initial in hearts subject to ischemia and 100% of initial nonischemic hearts.

Example 5. Effect of Morphogen on Neutrophil Adherence

[0103] The role of neutrophil adherence in endothelium dysfunction and the cardioprotective effects of morphogens in modulating this activity can be assessed using a standard polymorphonuclear neutrophil (PMN) adherence assay such as described in Lefer et al., (1992) *J. Mol. Cell. Cardiol.* **24**: 385-393. Briefly, segments of superior mesenteric artery were isolated from rats which had either been treated with morphogen (OP-1, 20 μ g) or 0.9% NaCl, 24 h prior to isolation of the artery. The segments were cleaned, cut into transverse rings of 1-2mm in length, and these were subsequently cut open and incubated in K-H solution at 37°C, pH 7.4. Neutrophils were prepared and fluorescently labelled using standard procedures (e.g., leukocytes were isolated from rats essentially following the procedure of Pertroff et. al. (1968) *Exp Cell Res* **50**: 355-368, washed in phosphate buffered saline (PBS), purified by gradient centrifugation; and labelled by the method of Yuan et. al. (1990) *Microvasc Res* **40**: 218-229..

[0104] Labelled neutrophils then were added to open ring baths and activated with 100nM leukotriene B₄ (LTB₄). Rings were incubated for 20 minutes and the number of neutrophils adhering to the endothelial surface then determined visually by fluorescent microscopy.

[0105] As shown in Figure 3, unstimulated PMNs (i.e., PMNS alone) added to the baths did not significantly adhere to the vascular endothelium. In rings taken from rats injected with 0.9% NaCl, activation of neutrophils with LTB₄ (100 nM) greatly increased the number of PMNs adherent to the endothelium ($P<0.001$). OP-1 (20 μ g administered 24 h prior) significantly inhibited adherence of PMNs activated by LTB₄ ($P<0.01$ from control).

Example 6. In Vivo Models for Ischemic-Reperfusion Protection in Lung, Nerve and Renal Tissue.

[0106] Other tissues seriously affected by ischemic-reperfusion injury include neural tissue, renal tissue and lung tissue. The effect of morphogens on alleviating the ischemic-reperfusion injury in these tissues may be assessed using methodologies and models known to those skilled in the art, and disclosed below. Similarly, a methodology also is provided for assessing the tissue-protective effects of a morphogen on damaged lung tissue following hyperoxia injury.

[0107] For example, the rabbit embolic stroke model provides a useful method for assessing the effect of morphogens on tissue injury following cerebral ischemia-reperfusion. The protocol disclosed below is essentially that of Phillips et al. (1989) *Annals of Neurology* **25**:281-285. Briefly, white New England rabbits (2-3kg) are anesthetized and placed on a respirator. The intracranial circulation then is selectively catheterized by the Seldinger technique. Baseline cerebral angiography then is performed, employing a digital substraction unit. The distal internal carotid artery or its branches then is selectively embolized with 0.035 ml of 18-hour-aged autologous thrombus. Arterial occlusion is documented by repeat angiography immediately after embolization. After a time sufficient to induce cerebral infarcts (15 minutes or 90

minutes), reperfusion is induced by administering a bolus of a reperfusion agent such as the TPA analogue Fb-FB-CF (e.g., 0.8 mg/kg over 2 minutes).

[0108] The effect of morphogen on cerebral infarcts can be assessed by administering varying concentrations of morphogens, e.g., OP1, at different times preceding or following embolization and/or reperfusion. The rabbits are sacrificed 3-14 days post embolization and their brains prepared for neuropathological examination by fixing by immersion in 10% neutral buffered formalin for at least 2 weeks. The brains then are sectioned in a coronal plane at 2-3 mm intervals, numbered and submitted for standard histological processing in paraffin, and the degree of neural tissue necrosis determined visually.

[0109] The renal-protective effects of morphogens on renal ischemia-reperfusion injury readily can be assessed 10 using the mouse model disclosed by Ouellette, et al. (1990), *J. Clin. Invest.* 85:766-771. Briefly, renal ischemia is induced surgically in 35-45 days old out-bred Swiss male mice by performing a standard right nephrectomy, and occluding the artery to the left kidney with a microaneurism clamp for 10-30 minutes. Morphogen then may be provided parentally, at various times prior to or following occlusion and/or reperfusion. The effects of morphogen then may be assessed by biological evaluation and histological evaluation using standard techniques well known in the art.

[0110] The tissue protective effects of morphogen on tissue exposed to lethally high oxygen concentrations may be 15 assessed by the following procedure. Adult rats (275-300 gms) first are provided with morphogen (e.g., hOP1) or vehicle only, and then are exposed to 96-98% oxygen essentially as described by Rinaldo et al (1983) *Am. Rev. Respir. Dis.* 130:1065, to induce hyperoxia. Animals are housed in plastic cages (38 cm x 48 xm x 21 cm). A cage containing 4-5 animals is placed in a 75 liter water-sealed plexiglass chamber. An atmosphere of 96-98% oxygen then is maintained 20 by delivery of O₂ gas (liquid O₂). Gas flow through the chamber is adjusted to maintain at least 10 air changes/hr., temperature at 22 ± 1°C, minimal levels of condensation within the cage, and carbon dioxide concentration of < 0.5% as measured with a mass spectrophotometric medical gas analyzer.

[0111] At the end of 72 hours all survivors are observed at room air for 1.5 hours and at longer time periods to 25 assess degree of respiratory distress and cyanosis induced by the initial insult and subsequent immune cell-mediated damage. The number of survivors at the end of the challenge is recorded and the treated groups compared with the untreated control group by chi-square test of proportions. Several of the surviving animals for each group are randomly chosen for histological processing of lung tissue.

[0112] Lung tissue for histological processing is fixed by infusion of 10% buffered formalin through a tracheal cannula at a constant pressure of 20 cm H₂O. After fixation for 24-48 hours, sections from each lobe are cut and subsequently stained with hematoxylin and eosin. Coded slides then are examined, preferably in a double-blind fashion for evidence of pathological changes such as edema, interstitial cellularity, and inflammatory response.

Example 7. Morphogen Inhibition of Cellular and Humoral Inflammatory Response

[0113] Morphogens described herein inhibit multinucleation of mononuclear phagocytic cells under conditions 35 where these cells normally would be activated, e.g., in response to a tissue injury or the presence of a foreign substance. For example, in the absence of morphogen, an implanted substrate material (e.g., implanted subcutaneously) composed of, for example, mineralized bone, a ceramic such as titanium oxide or any other substrate that provokes multinucleated giant cell formation, rapidly becomes surrounded by multinucleated giant cells, e.g., activated phagocytes stimulated to respond and destroy the foreign object. In the presence of morphogen however, the recruited cells remain in their mononuclear precursor form and the matrix material is undisturbed. Figure 4 illustrates this effect of morphogens, in a schematic representation of histology results of a titanium oxide substrate implanted subcutaneously. In 40 the figure, "mg" means mononuclear giant cells and "ob" means osteoblasts. The substrate represented in Fig. 4B was implanted together with morphogen (OP-1) and newly formed osteoblasts are evident surrounding the substrate. By contrast, the substrate represented in Fig. 4A was implanted without morphogen and extensive multinucleated giant cell 45 formation is evident surrounding the substrate. Accordingly, the morphogens' effect in inhibiting excessive bone mass loss in a mammal also may include inhibiting activation of these cells.

[0114] In addition, the morphogens described herein also suppress antibody production stimulated in response to 50 a foreign antigen in a mammal. Specifically, when bovine bone collagen matrix alone was implanted in a bony site in a rat, a standard antibody response to the collagen is stimulated in the rat as determined by standard anti-bovine collagen ELISA experiments performed on blood samples taken at four week intervals following implantation (e.g., between 12 and 20 weeks.) Serum anti-collagen antibody titers, measured by ELISA essentially following the procedure described by Nagler-Anderson et al, (1986) *PNAS* 83:7443-7446, increased consistently throughout the experiment. However, when the matrix was implanted together with a morphogen (e.g., OP-1, dispersed in the matrix and adsorbed thereto, 55 essentially as described in U.S. Pat. No. 4,968,590) anti-bovine collagen antibody production was suppressed significantly. This ability of morphogen to suppress the humoral response is further evidence of morphogen utility in alleviating tissue damage associated with autoimmune diseases, including autoantibody diseases, such as rheumatoid arthritis.

Example 8. Morphogen protection of Gastrointestinal Tract Mucosa from Ulceration and Inflammation

[0115] Oral mucositis is a gastrointestinal tract inflammatory disease which involves ulcerations of the mouth mucosa as a consequence of, e.g., radiation therapy or chemotherapy. While not typically a chronic disease, the tissue destructive effects of oral mucositis mirror those of chronic inflammatory diseases such as IBD. The example below demonstrates morphogen efficacy in protecting the oral mucosa from oral mucositis in a hamster model, including both inhibiting inflammatory ulceration and enhancing regeneration of ulcerated tissue. Details of the protocol can be found in Sonis, et al., (1990) *Oral Surg. Oral Med. Oral Pathol* 69: 437-443. Based on these data, the morphogens described herein should be efficacious in treating chronic inflammatory diseases including IBD, arthritis, psoriasis and psoriatic 10 arthritis, multiple sclerosis, and the like.

[0116] Golden syrian hamsters (6-8 wks old, Charles River Laboratories, Wilmington, MA) were divided into 3 test groups: Group 1, a placebo (e.g., saline) control, and a morphogen low dose group (100 ng) and a morphogen high dose group (1 µg). Groups 2 and 3, respectively. Morphogen dosages were provided in 30% ethanol. Each group contained 12 animals.

[0117] Beginning on day 0 and continuing through day 5, Groups 2 and 3 received twice daily morphogen applications. On day 3, all groups began the mucositis-induction procedure. 5-fluorouracil (60 mg/kg) was injected intraperitoneally on days 3 and 5. On day 7, the right buccal pouch mucosa was superficially irritated with a calibrated 18 gauge needle. In untreated animals, severe ulcerative mucositis was induced in at least 80% of the animals by day 10.

[0118] For each administration of the vehicle control (placebo) or morphogen, administration was performed by first gently drying the cheek pouch mucosa, then providing an even application over the mucosal surface of the vehicle or morphogen material. A hydroxypropylcellulose-based coating was used to maintain contact of the morphogen with the mucosa. This coating provided at least 4 hours of contact time.

[0119] On day 12, two animals in each group were sacrificed for histological studies. The right buccal pouch mucosa and underlying connective tissue were dissected and fixed in 10% formalin using standard dissection and histology procedures. The specimens were mounted in paraffin and prepared for histologic examination. Sections then were stained with hematoxylin and eosin and were examined blindly by three oral pathologists with expertise in hamster histology and scored blind against a standard mucositis panel. The extent of atrophy, cellular infiltration, connective tissue breakdown, degree of ulceration and epithelialization were assessed.

[0120] The mean mucositis score for each group was determined daily for each experimental group for a period of 21 days by photography and visual examination of the right buccal cheek pouch. Differences between groups were determined using a standard 't' test, e.g., the Students' 't' test. In addition, data was evaluated between groups by comparing the numbers of animals with severe mucositis using Chi Square statistical analysis. The significance of differences in mean daily weights also was determined.

[0121] The experimental results are presented in Fig. 5, which graphs the effect of morphogen (high dose, squares; low dose, diamonds) and placebo (circles) on mean mucositis scores. Both low and high morphogen doses inhibit lesion formation significantly in a dose-dependent manner. In addition, histology results consistently showed significantly reduced amounts of tissue atrophy, cellular debris, and immune effector cells, including macrophages and activated neutrophils, in the morphogen-treated animals, as compared with the untreated, control animals.

40 Example 9. Morphogen Effect on Fibrogenesis and Scar Tissue Formation

[0122] The morphogens described herein induce tissue morphogenesis of damaged or lost tissue. The ability of these proteins to regenerate new tissue enhances the anti-inflammatory effect of these proteins. Provided below are a series of in vitro experiments demonstrating the ability of morphogens to induce migration and accumulation of mesenchymal cells. In addition, the experiments demonstrate that morphogens, unlike TGF-β, do not stimulate fibrogenesis or scar tissue formation. Specifically, morphogens do not stimulate production of collagen, hyaluronic acid (HA) or metalloproteinases in primary fibroblasts, all of which are required for fibrogenesis or scar tissue formation. By contrast, TGF-β, a known inducer of fibrosis, but not of tissue morphogenesis, does stimulate production of these fibrosis markers.

[0123] Chemotaxis and migration of mesenchymal progenitor cells were measured in modified Boyden chambers essentially as described by Fava, R.A. et al (1991) *J. Exp. Med.* 173: 1121-1132, using polycarbonate filters of 2, 3 and 8 micron ports to measure migration of progenitor neutrophils, monocytes and fibroblasts. Chemotaxis was measured over a range of morphogen concentrations, e.g., 10^{-20} M to 10^{-12} M OP-1. For progenitor neutrophils and monocytes, 10^{-18} - 10^{-17} M OP-1 consistently induced maximal migration, and 10^{-14} to 10^{-13} M OP-1 maximally induced migration of progenitor fibroblasts. In all cases the chemotactic activity could be inhibited with anti-OP-1 antibody. Similar migration activities also were measured and observed with TGF-β.

[0124] The effect of morphogen on fibrogenesis was determined by evaluating fibroblast production of hyaluronic acid (HA), collagen, collagenase and tissue inhibitor of metalloproteinases (TIMP).

[0125] Human fibroblasts were established from explants of infant foreskins and maintained in monolayer culture using standard culturing procedures. (See, for example, (1976) *J. Exp. Med.* 144: 1188-1203.) Briefly, fibroblasts were grown in maintenance medium consisting of Eagle's MEM, supplemented with nonessential amino acids, ascorbic acid (50 µg/ml), NaHCO₃ and HEPES buffers (pH 7.2), penicillin (100 U/ml), streptomycin (100 µg/ml), amphotericin B (1 µg/ml) and 9% heat inactivated FCS. Fibroblasts used as target cells to measure chemotaxis were maintained in 150 mm diameter glass petri dishes. Fibroblasts used in assays to measure synthesis of collagen, hyaluronic acid, collagenase and tissue inhibitors of metalloproteinases (TIMP) were grown in 100 mm diameter plastic tissue culture petri dishes.

[0126] The effects of morphogen on fibroblast production of hyaluronic acid, collagens, collagenase and TIMP were determined by standard assays (See, for example, Postlethwaite et al. (1989) *J. Clin. Invest.* 83: 629-636, Postlethwaite (1988) *J. Cell Biol.* 106: 311-318 and Clark et al (1985) *Arch. Bio-chem Biophys.* 241: 36-44). For these assays, fibroblasts were transferred to 24-well tissue culture plates at a density of 8 x 10⁴ cells per well. Fibroblasts were grown confluence in maintenance medium containing 9% FCS for 72 h and then grown in serum-free maintenance medium for 24 h. Medium was then removed from each well and various concentrations of OP-1 (recombinantly produced mature or soluble form) or TGF-β-1 (R&D Systems, Minneapolis) in 50 µl PBS were added to triplicate wells containing the confluent fibroblast monolayers. For experiments that measured production of collagenase and TIMP, maintenance medium (450 µl) containing 5% FCS was added to each well, and culture supernatants were harvested from each well 48 h later and stored at -70°C until assayed. For experiments that assessed HA production, maintenance medium (450 µl) containing 2.5% FCS was added to each well, and cultures grown for 48 h. For experiments that measured fibroblast production of collagens, serum-free maintenance medium (450 µl) without non-essential amino acids was added to each well and cultures grown for 72 h. Fibroblast production of HA was measured by labeling newly synthesized glycosaminoglycans (GAG) with [³H]-acetate the last 24 h of culture and quantitating released radioactivity after incubation with hyaluronidase from *Streptomyces hyalurolyticus* (ICN Biochemicals, Cleveland, OH) which specifically degrades hyaluronic acid. Production of total collagen by fibroblasts was measured using a collagenase-sensitive protein assay that reflects [³H]-proline incorporation the last 24 h of culture into newly synthesized collagens. Collagenase and TIMP protein levels in fibroblast cultures supernatants was measured by specific ELISAs.

[0127] As shown in Fig. 6, OP1 does not stimulate significant collagen or HA production, as compared with TGF-β. In the figure, panel A shows OP-1 effect on collagen production, panel B shows TGF-β effect on collagen production, and panels C and D show OP-1 (panel C) and TGF-β (panel D) effect on HA production. The morphogen results were the same whether the soluble or mature form of OP1 was used. By contrast, the latent form of TGF-β (e.g., pro domain-associated form of TGF-β) was not active.

Example 10. Morphogen Inhibition of Epithelial Cell Proliferation

[0128] This example demonstrates the ability of morphogens to inhibit epithelial cell proliferation *in vitro*, as determined by ³H-thymidine uptake using culture cells from a mink lung epithelial cell line (ATCC No. CCL 64), and standard mammalian cell culturing procedures. Briefly, cells were grown to confluence in Eagle's minimum essential medium (EMEM) supplemented with 10% fetal bovine serum (FBS), 200 units/ml penicillin, and 200 µg/ml streptomycin, and used to seed a 48-well cell culture plate at a cell density of 200,000 cells per well. When this culture became confluent, the media was replaced with 0.5 ml of EMEM containing 1% FBS and penicillin/streptomycin and the culture incubated for 24 hours at 37°C. Morphogen test samples in EMEM containing 5% FBS then were added to the wells, and the cells incubated for another 18 hours. After incubation, 1.0 µCi of ³H-thymidine in 10 µl was added to each well, and the cells incubated for four hours at 37°C. The media then was removed and the cells washed once with ice-cold phosphate-buffer saline and DNA precipitated by adding 0.5 ml of 10% TCA to each well and incubating at room temperature of 15 minutes. The cells then were washed three times with ice-cold distilled water, lysed with 0.5 ml 0.4 M NaOH, and the lysate from each well then transferred to a scintillation vial and the radioactivity recorded using a scintillation counter (Smith-Kline Beckman).

[0129] The results are presented in Table III, below. The anti-proliferative effect of the various morphogens tested was expressed as the counts of ³H-thymidine (x 1000) integrated into DNA, and were compared with untreated cells (negative control) and TGF-β (1 ng), a local-acting factor also known to inhibit epithelial cell proliferation. COP-5 and COP-7 are biosynthetic constructs that previously have been shown to have osteogenic activity, capable of inducing the complete cascade resulting in endochondral bone formation in a standard rat bone assay (see U.S. Pat. No. 5,011,691.) The morphogens significantly inhibit epithelial cell proliferation. Similar experiments, performed with the morphogens COP-16, bOP (bone-purified osteogenic protein, a dimeric protein comprising CBMP2 and OP-1), and recombinant OP-1, also inhibit cell proliferation. bOP and COP-16 also induce endochondral bone formation (see US Pat. No. 4,968,590 and 5,011,691.)

TABLE III

	Thymidine uptake (x 1000)
control	50.048, 53.692
COP-7-1 (10 ng)	11.874
COP-7-2 (3 ng)	11.136
COP-5-1 (66 ng)	16.094
COP-5-2 (164 ng)	14.43
TGF- β (1 ng)	1.86, 1.478

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Example 11. Morphogen Treatment of a Systemic Inflammatory Disease

[0130] The following example provides a rat adjuvant-induced arthritis model for demonstrating morphogen efficacy in treating arthritis and other systemic inflammatory diseases. Rat adjuvant-induced arthritis induces a systemic inflammatory disease with bone and cartilage changes similar to those observed in rheumatoid arthritis, but in an accelerated time span (see, for example, Pearson (1964) *Arth. Rheum.* 7:80). A detailed description of the protocol is provided in Walz, et al., (1971) *J. Pharmac. Exp. Ther.* 178: 223-231.

[0131] Briefly, Sprague-Dawley female rats (e.g., Charles River Laboratories, Wilmington, MA) are randomized into 3 groups: control; morphogen, low dose (e.g., 1-10 μ g/kg weight per day) and morphogen, high dose (e.g., 10-20 μ g/kg weight per day), referred to as Groups 1, 2, and 3, respectively.

[0132] Adjuvant arthritis is induced in all three groups by injection of 0.05 ml of a suspension of 1.5% dead *Mycobacterium butyricum* in mineral oil into the subplantar surface of the right hind paw. On Day 18 after adjuvant injection, the limb volumes of both hind limb are determined. In the absence of morphogen treatment, a systemic arthritic condition is induced in adjuvant-injected rats by this time, as determined by significant swelling of the uninjected hind limbs (< 2.3 ml, volume measured by mercury displacement). Subsequent determinations of paw edema and x-ray scores are made on the uninjected hind limb. Rats in Group 2 and 3 also are dosed orally daily, beginning on Day 1, with morphogen. Limb volumes are recorded on Days 29 and 50 after adjuvant injection and edema determined by volume difference compared to Day 18. The uninjected hind limb on each rat is x-rayed on Day 50 and the joint damage assayed on an arbitrary scale of 1 to 10 (1=no damage, 10=maximum damage). Data on differences between control and treated groups (Day 29 edema, Day 50 edema and Day 50 x-ray scores) are analyzed by using a standard "t-test. Morphogen-treated rats show consistently reduced joint damage (e.g., decreased in edema and in x-ray scores) as compared with untreated control rats.

[0133] As another, alternative example, Groups 2 and 3 are dosed daily with morphogen beginning on Day 18 and continuing through Day 50 to demonstrate the efficacy of morphogens in arthritic animals.

Example 12. Morphogen Inhibition of Localized Edema

[0134] The following example demonstrates morphogen efficacy in inhibiting a localized inflammatory response in a standard rat edema model. Experimental rats (e.g., Long-Evans from Charles River Laboratories, Wilmington, MA) are divided into three groups: Group 1, a negative control, which receives vehicle alone; Group 2, a positive control, to which is administered a well-known characterized anti-inflammatory agent (e.g., indomethacin), and Group 3, to which morphogen is provided.

[0135] Groups 2 and 3 may be further subdivided to test low, medium and high doses (e.g., Group 2: 1.0 mg/kg, 3.0 mg/kg and 9.0 mg/kg indomethacin; Group 3: 0.1-5 μ g, 5-20 μ g, and 20-50 μ g of morphogen). Sixty minutes after indomethacin or morphogen is provided to the rats of Group 2 or 3 (e.g., as by injection into the tail vein, or by oral gavage) inflammation is induced in all rats by a sub-plantar injection of a 1% carrageenin solution (50 μ l) into the right hind paw. Three hours after carrageenin administration paw thickness is measured as an indication of edema (e.g., swelling) and induced inflammatory response to the injected carrageenin solution.

[0136] Significant swelling is evident in untreated rats by three hours after carrageenin injection. Inflammation also is measured by histology by standard means, following euthanasia e.g.: the right hind paw from each animal is removed at the ankle joint and weighed and foot pad tissue is fixed in 10% neutral buffered formalin, and slides prepared for visual examination by staining the prepared tissue with hematoxylin and eosin.

[0137] The morphogen-treated rats show substantially reduced edema induction following carrageenin injection as compared with the untreated rats.

Example 13. Morphogen Treatment of Allergic Encephalomyelitis

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[0138] The following example demonstrates morphogen efficacy in treating experimental allergic encephalomyelitis (EAE) in a rat. EAE is a well-characterized animal model for multiple sclerosis, an autoimmune disease. A detailed description of the protocol is disclosed in Kuruvilla, et al., (1991) *PNAS* 88:2918-2921.

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[0139] Briefly, EAE is induced in rats (e.g., Long-Evans, Charles River Laboratories, Wilmington, MA) by injection of a CNS tissue (e.g., spinal cord) homogenate in complete Freund's adjuvant (CFA) on days -44, -30 and 0 (last day of immunization), by subcutaneous injection to three sites on the animal's back. Morphogen is administered daily by interperitoneal injection beginning on day -31. Preferably, a series of morphogen dose ranges is evaluated (e.g., low, medium and high) as for Example 12, above.) Control rats receive morphogen vehicle only (e.g. 0.9% NaCl or buffered saline). Rats are examined daily for signs of disease and graded on an increasing severity scale of 0-4.

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[0140] In the absence of morphogen treatment, significant neurological dysfunction (e.g., hind and fore limb weakness, progressing to total hind limb paralysis) is evident by day +7 to +10. Hematology, serum chemistry profiles and histology are performed to evaluate the degree of tissue necropsy using standard procedures. Morphogen treatment significantly inhibits the neurological dysfunction normally evident in an EAE animal. In addition, the histopathological markers typically associated with EAE are absent in the morphogen-treated animals

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Example 14. Morphogen Treatment of Collagen-Induced Arthritis

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[0141] The following example demonstrates the efficacy of morphogens in inhibiting the inflammatory response in a collagen-induced arthritis (CIA) in a rat. CIA is a well-characterized animal model for rheumatoid arthritis, an autoimmune disease. The protocol disclosed is essentially that disclosed in Kuruvilla et al., (1991) *PNAS* 88:2918-2921. Briefly, CIA is induced in experimental rats (e.g., Long-Evans, Charles River Laboratories, Wilmington), by multiple intradermal injection of bovine Type II collagen (e.g., 100 μ g) in CFA (0.2 ml) on Day 1. Animals are divided into two groups: Group 1, control animals, which receive vehicle alone, and Group 2: morphogen-treated animals, which, preferably, are subdivided into low, medium and high dose ranges, as described for Example 13, above. Morphogen is administered daily (e.g., by tail vein injection) beginning at different times following collagen injection, e.g., beginning on day 7, 14, 28, 35 and 42. Animals are evaluated visually and paw thickness and body weight is monitored throughout the experiment. Animals are sacrificed on day 60 and the proximal and distal limb joints, and ear, tail and spinal cord prepared for histological evaluation as described for Examples 12 and 13, above. In a variation of the experiment, morphogen may be administered for prescribed periods, e.g., five day periods, beginning at different times following collagen injection (e.g., on days 0-4, 7-11, 14-18, 28-32.)

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[0142] In the absence of morphogen treatment, an arthritic condition typically is induced by 30 days post collagen injection. In morphogen-treated animals, CIA is suppressed and the histopathological changes typically evidenced in control CIA-induced animals are absent: e.g., accumulations of activated mononuclear inflammatory cells and fibrous connective tissue. In addition, consistent with the results in Example 7, above, serum anti-collagen antibody titers are suppressed significantly in the morphogen-treated animals.

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Example 15. Screening Assay for Candidate Compounds which Alter Endogenous Morphogen Levels

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[0143] Candidate compound(s) which may be administered to affect the level of a given morphogen may be found using the following screening assay, in which the level of morphogen production by a cell type which produces measurable levels of the morphogen is determined with and without incubating the cell in culture with the compound, in order to assess the effects of the compound on the cell. This can be accomplished by detection of the morphogen either at the protein or RNA level. A more detailed description also may be found in USSN 752,861.

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15.1 Growth of Cells in Culture

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[0144] Cell cultures of kidney, adrenals, urinary bladder, brain, or other organs, may be prepared as described widely in the literature. For example, kidneys may be explanted from neonatal or new born or young or adult rodents (mouse or rat) and used in organ culture as whole or sliced (1-4 mm) tissues. Primary tissue cultures and established cell lines, also derived from kidney, adrenals, urinary, bladder, brain, mammary, or other tissues may be established in multiwell plates (6 well or 24 well) according to conventional cell culture techniques, and are cultured in the absence or presence of serum for a period of time (1-7 days). Cells may be cultured, for example, in Dulbecco's Modified Eagle medium (Gibco, Long Island, NY) containing serum (e.g., fetal calf serum at 1%-10%, Gibco) or in serum-deprived

medium, as desired, or in defined medium (e.g., containing insulin, transferrin, glucose, albumin, or other growth factors).

[0145] Samples for testing the level of morphogen production includes culture supernatants or cell lysates, collected periodically and evaluated for OP-1 production by immunoblot analysis (Sambrook et al., eds., 1989, Molecular Cloning, Cold Spring Harbor Press, Cold Spring Harbor, NY), or a portion of the cell culture itself, collected periodically and used to prepare polyA+ RNA for RNA analysis. To monitor *de novo* OP-1 synthesis, some cultures are labeled according to conventional procedures with an ^{35}S -methionine/ ^{35}S -cysteine mixture for 6-24 hours and then evaluated to OP-1 synthesis by conventional immunoprecipitation methods.

10 15.2 Determination of Level of Morphogenic Protein

[0146] In order to quantitate the production of a morphogenic protein by a cell type, an immunoassay may be performed to detect the morphogen using a polyclonal or monoclonal antibody specific for that protein. For example, OP-1 may be detected using a polyclonal antibody specific for OP-1 in an ELISA, as follows.

[0147] 1 $\mu\text{g}/100 \mu\text{l}$ of affinity-purified polyclonal rabbit IgG specific for OP-1 is added to each well of a 96-well plate and incubated at 37°C for an hour. The wells are washed four times with 0.167M sodium borate buffer with 0.15 M NaCl (BSB), pH 8.2, containing 0.1% Tween 20™. To minimize non-specific binding, the wells are blocked by filling completely with 1% bovine serum albumin (BSA) in BSB and incubating for 1 hour at 37°C. The wells are then washed four times with BSB containing 0.1% Tween 20. A 100 μl aliquot of an appropriate dilution of each of the test samples of cell culture supernatant is added to each well in triplicate and incubated at 37°C for 30 min. After incubation, 100 μl biotinylated rabbit anti-OP-1 serum (stock solution is about 1 mg/ml and diluted 1:400 in BSB containing 1% BSA before use) is added to each well and incubated at 37°C for 30 min. The wells are then washed four times with BSB containing 0.1% Tween 20. 100 μl streptavidin-alkaline (Southern Biotechnology Associates, Inc. Birmingham, Alabama, diluted 1:2000 in BSB containing 0.1% Tween 20 before use) is added to each well and incubated at 37°C for 30 min. The plates are washed four times with 0.5M Tris buffered Saline (TBS), pH 7.2. 50 μl substrate (ELISA Amplification System Kit, Life Technologies, Inc., Bethesda, MD) is added to each well incubated at room temperature for 15 min. Then, 50 μl amplifier (from the same amplification system kit) is added and incubated for another 15 min at room temperature. The reaction is stopped by the addition of 50 μl 0.3 M sulphuric acid. The OD at 490 nm of the solution in each well is recorded. To quantitate OP-1 in culture media, a OP-1 standard curve is performed in parallel with the test samples.

[0148] Polyclonal antibody may be prepared as follows. Each rabbit is given a primary immunization of 100 $\mu\text{g}/500 \mu\text{l}$ E. coli produced OP-1 monomer (amino acids 328-431 in SEQ ID NO:5) in 0.1% SDS mixed with 500 μl Complete Freund's Adjuvant. The antigen is injected subcutaneously at multiple sites on the back and flanks of the animal. The rabbit is boosted after a month in the same manner using incomplete Freund's Adjuvant. Test bleeds are taken from the ear vein seven days later. Two additional boosts and test bleeds are performed at monthly intervals until antibody against OP-1 is detected in the serum using an ELISA assay. Then, the rabbit is boosted monthly with 100 μg of antigen and bled (15 ml per bleed) at days seven and ten after boosting.

[0149] Monoclonal antibody specific for a given morphogen may be prepared as follows. A mouse is given two injections of E. coli produced OP-1 monomer. The first injection contains 100 μg of OP-1 in complete Freund's adjuvant and is given subcutaneously. The second injection contains 50 μg of OP-1 in incomplete adjuvant and is given intraperitoneally. The mouse then receives a total of 230 μg of OP-1 (amino acids 307-431 in SEQ ID NO:5) in four intraperitoneal injections at various times over an eight month period. One week prior to fusion, both mice are boosted intraperitoneally with 100 μg of OP-1 (307-431) and 30 μg of the N-terminal peptide (Ser₂₉₃-Asn₃₀₉-Cys) conjugated through the added cysteine to bovine serum albumin with SMCC crosslinking agent. This boost was repeated five days (IP), four days (IP), three days (IP) and one day (IV) prior to fusion. The mouse spleen cells are then fused to myeloma (e.g., 653) cells at a ratio of 1:1 using PEG 1500 (Boehringer Mannheim), and the cell fusion is plated and screened for OP-1-specific antibodies using OP-1 (307-431) as antigen. The cell fusion and monoclonal screening then are according to standard procedures well described in standard texts widely available in the art.

[0150] The invention may be embodied in other specific forms and the present embodiments are therefore to be considered in all respects as illustrative and not restrictive, the scope of the invention being indicated by the appended claims.

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT: KUBERASAMPATH, THANGAVEL
PANG, ROY H.L.
OPPERMANN, HERMANN
RUEGER, DAVID C.
COHEN, CHARLES M.
OZKAYNAK, ENGIN
SMART, JOHN

10

(ii) TITLE OF INVENTION: MORPHOGEN-INDUCED MODULATION OF
15 INFLAMMATORY RESPONSE

15

(iii) NUMBER OF SEQUENCES: 33

20

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CREATIVE BIOMOLECULES
(B) STREET: 35 SOUTH STREET
(C) CITY: HOPKINTON
(D) STATE: MASSACHUSETTS
(E) COUNTRY: U.S.A.
(F) ZIP:

25

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25

30

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 667,274
(B) FILING DATE: 11-MAR-1991

35

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 753,059
(B) FILING DATE: 30-AUG-1991

40

(viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 752,764
(B) FILING DATE: 30-AUG-1991
(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

50

55

(ix) FEATURE:

(A) NAME: Generic Sequence 1
 (D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	Xaa Xaa Xaa Xaa Xaa Xaa	
10	1	5
	Xaa	
	10	15
15	Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa	
	20	25
	Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
	30	35
20	Xaa	
	40	45
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys	
	55	60
25	Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
	65	70
	Xaa	
	75	80
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys	
	85	90
	Xaa Cys Xaa	
	95	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 2
 (D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Xaa Xaa Xaa Xaa Xaa Xaa	
45	1	5
	Xaa	
	10	15
50	Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa	
	20	25
	Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa	
	30	35
55	Xaa	
	40	45
	50	

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 5 55 60
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70
 Xaa
 75 80
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 85 90
 10 Xaa Cys Xaa
 95

(2) INFORMATION FOR SEQ ID NO:3:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: Generic Sequence 3
 (D) OTHER INFORMATION: wherein each
 20 Xaa is independently selected from
 a group of one or more specified
 amino acids as defined in the
 specification.

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Tyr Val Xaa Phe
 30 1 5
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 10
 Xaa Ala Pro Gly Xaa Xaa Xaa Ala
 15 20
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 25 30
 Xaa Pro Xaa Xaa Xaa Xaa Xaa
 35
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 40 45
 Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
 50
 Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55 60
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 65
 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70 75
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 80
 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 85 90
 55 Xaa Cys Gly Cys Xaa
 95

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: Generic Sequence 4
 - (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
1				5					10
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
				15					
Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala		
20					25				
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
		30				35			
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa			
				40					
Asn	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa		
			45			50			
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa		
				55					
Xaa	Cys								
	60				65				
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa		
			70						
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa			
	75				80				
Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa		
				85					
Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa		
	90				95				
Xaa	Cys	Gly	Cys	Xaa					
			100						

INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: hOP-1 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln
	1				5				
	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
	10					15			
	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala
							25		
10	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
			30					35	
	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40						45
15	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
					50				
	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
20		65				70			
	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
			75					80	
	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85						90
25	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
					95				
	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	100					105			
	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
		110					115		
30	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
			120					125	
	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130						135
	Cys	Gly	Cys	His					

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: mOP-1 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

45	Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln
	1				5				
	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
	10					15			
	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala
							25		
50	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
			30					35	

5	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40						45
	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
					50				
	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
			55			60			
10	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
			65			70			
	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
			75					80	
	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85						90
15	Val	His	Phe	Ile	Asn	Pro	Asp	Thr	Val
			95						
	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	100					105			
	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
		110					115		
20	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
			120					125	
	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130						135
	Cys	Gly	Cys	His					

(2)

INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: hOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
	1				5				
	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
		10				15			
40	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
		20					25		
	Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
			30					35	
	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40						45
45	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
					50				
	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
		55				60			
50	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
			65				70		
	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			75						

5	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
				85					90
	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
					95				
	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
	100					105			
10	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
							115		
	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
				120				125	
	Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
				130					135
15	Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: mOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25	Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
	1				5				
	Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
						15			
30	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
		20					25		
	Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
			30					35	
35	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40						45
	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
					50				
40	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
		55				60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
		65					70		
45	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
			75					80	
	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
				85					90
50	Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
					95				
	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
	100					105			
	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		110					115		
	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
			120					125	

Lys His Arg Asn Met Val Val Lys Ala
 130 135
 Cys Gly Cys His

5

(2)

INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: CBMP-2A(fx)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser
 1 5 10
 Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
 15 20
 Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu
 25 30
 Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser
 35 40
 Thr Asn His Ala Ile Val Gln Thr Leu Val Asn
 45 55
 Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
 60 65
 Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 70 75
 Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys
 80 85
 Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
 90 95
 Cys Arg
 100

35

(2)

INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: CBMP-2B(fx)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40

Cys Arg Arg His Ser
 1 5
 Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala
 20 25

45

50

Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu
 30 35
 Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
 40 45
 Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser
 50 55 60
 Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu
 65 70
 Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Tyr
 75 80
 Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 85 90
 Val Val Glu Gly Cys Gly Cys Arg
 95 100

5

10

15

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: DPP(fx)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

20

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45

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser
 1 5 10
 Asp Val Gly Trp Asp Asp Trp Ile Val Ala Pro
 15 20
 Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly Lys
 25 30
 Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser
 35 40
 Thr Asn His Ala Val Val Gln Thr Leu Val Asn
 45 50 55
 Asn Asn Asn Pro Gly Lys Val Pro Lys Ala Cys
 60 65
 Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met
 70 75
 Leu Tyr Leu Asn Asp Gln Ser Thr Val Val Leu
 80 85
 Lys Asn Tyr Gln Glu Met Thr Val Val Gly Cys
 90 95
 Gly Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

50

55

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(ix) FEATURE:
 (A) NAME: Vgl(fx)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys
 1 5 10
 Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro
 15 20
 10 Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu
 25 30
 Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly
 35 40
 Ser Asn His Ala Ile Leu Gln Thr Leu Val His
 45 50 55
 Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys
 60 65
 Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met
 70 75
 20 Leu Phe Tyr Asp Asn Asn Asp Asn Val Val Leu
 80 85
 Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys
 90 95
 Gly Cys Arg
 25 100

(2)

INFORMATION FOR SEQ ID NO:13:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 30 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:
 (A) NAME: Vgr-1(fx)
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln
 1 5 10
 Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro
 40 15 20
 Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu
 25 30
 Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
 35 40
 Thr Asn His Ala Ile Val Gln Thr Leu Val His
 45 50 55
 Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys
 60 65
 Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val
 50 70 75

5
 Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu
 80 85
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys
 90 95
 Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:14:

10
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: protein
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

15
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (F) TISSUE TYPE: BRAIN

20
 (ix) FEATURE:
 (D) OTHER INFORMATION:
 /product= "GDF-1 (fx)"

25
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly
 1 5 10

30
 Trp His Arg Trp Val Ile Ala Pro Arg Gly Phe Leu Ala Asn Tyr
 15 20 25

35
 Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly
 30 35 40

40
 Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His
 45 50 55

45
 Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala
 60 65 70

50
 Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn
 75 80 85

55
 Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly
 90 95 100

50
 Cys Arg
 105

(2) INFORMATION FOR SEQ ID NO:15:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS
 (F) TISSUE TYPE: HIPPOCAMPUS

30 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (D) OTHER INFORMATION:/standard name= "hOP1"

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCCGGCGG ATG CAC GTG
 Met His Val
 1

57

40 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA
 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
 5 10 15

105

45 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC
 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
 20 25 30 35

153

50 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG
 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
 40 45 50

201

55

	CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg 55 60 65	249
5	CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met 70 75 80	297
10	CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGG CCC GGC Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly 85 90 95	345
15	GCC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly 100 105 110 115	393
20	CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp 120 125 130	441
25	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe 135 140 145	489
30	CAC CCA CGC TAC CAC CAT CGA GAG TTC CCG TTT GAT CTT TCC AAG ATC His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile 150 155 160	537
35	CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CCG ATC TAC AAG GAC Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp 165 170 175	585
40	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CCG ATC AGC GTT TAT Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr 180 185 190 195	633
45	CAG CTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu 200 205 210	681
50	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp 215 220 225	729
55	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu 230 235 240	777
55	GCC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro 245 250 255	825

	AAC TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275	873
5	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290	921
10	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305	969
15	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320	1017
20	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1065
25	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1113
30	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
35	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1209
40	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1257
45	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305
50	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420 425 430	1351
55	GAGAATTCAAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG GAACCAGCAG ACCAACTGCC TTTTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTT CAGTGGCAGC ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC	1411 1471 1531 1591

5	GCATAAAAGAA AAATGGCCGG GCCAGGTCA TGGCTGGAA GTCTCAGCCA TGCACGGACT	1651
	CGTTTCCAGA GGTAAATTATG AGCCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
	GGCGTGGCAA GGGGTGGCA CATGGTGTC TGTCGAAAG GAAAATTGAC CCGGAAGTTC	1771
	CTGTAATAAA TGTACAATA AACGAATGA ATGAAAAAAA AAAAAAAAAA A	1822

10 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (D) OTHER INFORMATION: /Product="OP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala			
1	5	10	15

25	Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser		
	20	25	30

30	Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser		
	35	40	45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu		
50	55	60

35	Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro			
	65	70	75	80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly		
85	90	95

40	Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser		
	100	105	110

45	Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr		
	115	120	125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys		
130	135	140

50	Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu			
	145	150	155	160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 5 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 10 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 15 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 20 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 25 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 30 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 35 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 40 355 360 365
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 45 385 390 395 400
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415
 50 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1873 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ii) MOLECULE TYPE: cDNA

vi) ORIGINAL SOURCE:
(A) ORGANISM: MURIDAE
(F) TISSUE TYPE: EMBRYO

ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 104..1393
(D) OTHER INFORMATION: /note= "MOP1 (cDNA)"

x) SEQUENCE DESCRIPTION: SEQ ID NO:18:

	CTGCAGCAAG	TGACCTCGGG	TCGTGGACCG	CTGCCCTGCC	CCCTCCGCTG	CCACCTGGGG	60
25	CGGCGCGGGC	CCGGTGCCCC	GGATCGCGCG	TAGAGCCGGC	GCG	ATG CAC GTG CGC	115
					Met	His Val Arg	
					1		
30	TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT	Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro	163				
	5	10	15	20			
35	CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG	Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu	211				
	25	30	35				
40	GTG CAC TCC AGC TTC ATC CAC CCG CGC CTC CGC AGC CAG GAG CGG CGG	Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg	259				
	40	45	50				
45	GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CGG	Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro	307				
	55	60	65				
50	CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG	Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu	355				
	70	75	80				
55	GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG	Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln	403				
	85	90	95	100			

	GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro 105 110 115	451
5	TTA GCC AGC CTG CAG GAC AGC CAT TTC CTC ACT GAC GCC GAC ATG GTC Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val 120 125 130	499
10	ATG AGC TTC GTC AAC CTA GTG GAA CAT GAC AAA GAA TTC TTC CAC CCT Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro 135 140 145	547
15	CGA TAC CAC CAT CGG GAG TTC CGG TTT GAT CTT TCC AAG ATC CCC GAG Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu 150 155 160	595
20	GGC GAA CGG GTG ACC GCA GCC GAA TTC AGG ATC TAT AAG GAC TAC ATC Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile 165 170 175 180	643
25	CGG GAG CGA TTT GAC AAC GAG ACC TTC CAG ATC ACA GTC TAT CAG GTG Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr Val Tyr Gln Val 185 190 195	691
30	CTC CAG GAG CAC TCA GGC AGG GAG TCG GAC CTC TTC TTG CTG GAC AGC Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser 200 205 210	739
35	CGC ACC ATC TGG GCT TCT GAG GAG GGC TGG TTG GTG TTT GAT ATC ACA Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr 215 220 225	787
40	GCC ACC AGC AAC CAC TGG GTG GTC AAC CCT CGG CAC AAC CTG GGC TTA Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu 230 235 240	835
45	CAG CTC TCT GTG GAG ACC CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu 245 250 255 260	883
50	GCA GGC CTG ATT GGA CGG CAT GGA CCC CAG AAC AAG CAA CCC TTC ATG Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met 265 270 275	931
	GTG GCC TTC TTC AAG GCC ACG GAA GTC CAT CTC CGT AGT ATC CGG TCC Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg Ser Ile Arg Ser 280 285 290	979
	ACG GGG GGC AAG CAG CGC AGC CAG AAT CGC TCC AAG ACG CCA AAG AAC Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn 295 300 305	1027

	CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp 310 315 320	1075
5	CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp 325 330 335 340	1123
10	CTT GGC TCG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr 345 350 355	1171
15	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala 360 365 370	1219
20	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp 375 380 385	1267
	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser 390 395 400	1315
25	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg 405 410 415 420	1363
30	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTTCTTG TGAGACCCCTG Asn Met Val Val Arg Ala Cys Gly Cys His 425 430	1413
	ACCTTTGGGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
35	CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACCC TCCCAACCGG	1533
	AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCTTCT	1593
40	GGCACGTGAC GGACAAGATC CTACCAAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
	GTCCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
	AATCGCAAGC CTCGTTCAAGC TGCAGCAGAA CGAAGGGCTT AGCCACGGTG GGGCGCTGGCG	1773
45	TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
	GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTG	1873

(2) INFORMATION FOR SEQ ID NO:19:

(1) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

15 (ix) FEATURE:
 (D) OTHER INFORMATION: /product= "mOP1-PP"

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
 85 90 95

Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
 100 105 110

Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
 115 120 125

Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
 130 135 140

Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
 145 150 155 160

Lys Ile Pro Glu Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr
 165 170 175

Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
 180 185 190

Val Tyr Gln Val Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
 195 200 205

Leu Leu Asp Ser Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val
 210 215 220
 5 Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His
 225 230 235 240
 Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile
 245 250 255
 10 Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys
 260 265 270
 Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg
 15 275 280 285
 Ser Ile Arg Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys
 290 295 300
 20 Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn
 305 310 315 320
 Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val
 325 330 335
 25 Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly
 340 345 350
 Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser
 355 360 365
 30 Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe
 370 375 380
 Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400
 Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415
 40 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:20:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1723 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(v1) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens
 (F) TISSUE TYPE: HIPPOCAMPUS

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(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 490..1696
 (D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCGCCGGCA	GAGCAGGAGT	GGCTGGAGGA	GCTGTGGTTG	GAGCAGGAGG	TGGCACGGCA	60	
15	GGGCTGGAGG	GCTCCCTATG	AGTGGCGGAG	ACGGCCCAGG	AGGCCTGGA	GAAACAGCTC	120
CCACACCGCA	CCAAGCGGTG	GCTGCAGGAG	CTCGCCCATC	GCCCCCTGCC	TGCTCGGACC	180	
20	GCGGCCACAG	CCGGACTGGC	GGGTACGGCG	GCGACAGAGG	CATTGGCCGA	GAGTCCCAGT	240
CCGCAGAGTA	CCCCCGGCCT	CGAGGCCGTG	GCGTCCCCTG	CCTCTCCGTC	CAGGAGCCAG	300	
25	GACAGGTGTC	GCCCGGCGGG	GCTCCAGGGA	CCGCGCCTGA	GGCCGGCTGC	CCGCGCGTCC	360
CGCCCCGCCC	CGCCGCCCCG	CGCCCGCCGA	GCCCAGCCTC	CTTGCCGTCG	GGGCGTCCCC	420	
AGGCCCTGGG	TCGGCCGCGG	AGCCGATGCG	CGCCCGCTGA	GCGCCCCAGC	TGAGCGCCCC	480	
30	CGGCCTGCC	ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu			528	
	1	5	10				
GCG CTA TGC GCG CTG GGC GGG GGC CCC GGC CTG CGA CCC CCG CCC						576	
Ala Leu Cys Ala Leu Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro	15	20	25				
35	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG					624	
Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln	30	35	40	45			
40	CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC					672	
Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	50	55	60				
45	GGC CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG					720	
Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	65	70	75				
50	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG					768	
Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	80	85	90				

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	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val 95 100 105	816
5	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp 110 115 120 125	864
10	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val 130 135 140	912
15	ACA GCT GCG GAG TTC CCG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu 145 150 155	960
20	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser 160 165 170	1008
25	AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala 175 180 185	1056
30	GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys 190 195 200 205	1104
35	TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu 210 215 220	1152
40	ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly 225 230 235	1200
45	CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg 240 245 250	1248
50	GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg 255 260 265	1296
55	AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu 270 275 280 285	1344
55	CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys 290 295 300	1392

	CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp 305 310 315	1440
5		
	TCG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu 320 325 330	1488
10		
	TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile 335 340 345	1536
15		
	CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala 350 355 360 365	1584
20		
	TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp 370 375 380	1632
25		
	AGC AGC AAC AAC GTC ATC CTG CGC AAA CAC CGC AAC ATG GTG GTC AAG Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys 385 390 395	1680
30		
	GCC TGC GGC TGC CAC T GAGTCAGCCCC GCCCAGCCCT ACTGCAG Ala Cys Gly Cys His 400	1723

30 (2) INFORMATION FOR SEQ ID NO:21:

- 35 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 402 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- 40 (ii) MOLECULE TYPE: protein
- 45 (ix) FEATURE:
 - (A) OTHER INFORMATION: /product= "hOP2-PP"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys 1 5 10 15		
45	Ala Leu Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro 20 25 30	
50	Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile 35 40 45	

	Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro			
	50	55	60	
5	Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu			
	65	70	75	80
	Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu			
	85	90	95	
10	Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val			
	100	105	110	
15	Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe			
	115	120	125	
	Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala			
	130	135	140	
20	Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr			
	145	150	155	160
	Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu			
	165	170	175	
25	Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu			
	180	185	190	
30	Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu			
	195	200	205	
	Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp			
	210	215	220	
35	Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala			
	225	230	235	240
	Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro			
	245	250	255	
40	Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln			
	260	265	270	
45	Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile			
	275	280	285	
	Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His			
	290	295	300	
50	Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile			
	305	310	315	320

Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335
 5 Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 340 345 350
 Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365
 10 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380
 Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400
 15 Cys His

(2) INFORMATION FOR SEQ ID NO:22:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1926 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: cDNA
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: MURIDAE
 (F) TISSUE TYPE: EMBRYO
 30 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 93..1289
 (D) OTHER INFORMATION: /note= "mOP2 cDNA"
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

40	CCGAGGCACA GGTGCGCCGT CTGGTCTTC CCGCTGGCG TCAGCCGAGC	50
	CCGACCAAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT	104
	Met Ala Met Arg	
	1	
45	CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC	152
	Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
	5 10 15 20	
50	GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA	200
	Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
	25 30 35	

	GCG CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly 40 45 50	248
5	CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln 55 60 65	296
10	CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr 70 75 80	344
15	GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp 85 90 95 100	392
20	CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly 105 110 115	440
25	TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile 120 125 130	488
30	CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CCG ATC TAC AAA GAA Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu 135 140 145	536
35	CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu 150 155 160	584
40	GTG GTC CAA GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp 165 170 175 180	632
45	CTT CAG ACG CTC CGA TCT GGG GAC GAG GCC TGG CTG CTG CTG GAC ATC Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile 185 190 195	680
50	ACA GCA GCC AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GGA Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly 200 205 210	728
55	CTC CGC CTC TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT CCT GGC Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly 215 220 225	776
55	CTG GCT GGT CTG CTT GGA CGA CAA GCA CCA CGC TCC AGA CAG CCT TTC Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe 230 235 240	824

	ATG GTA ACC TTC TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT CGG Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg 245 250 255 260	872
5	GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA AAG AAA ACG AAC GAG CTT Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu 265 270 275	920
10	CCG CAC CCC AAC AAA CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser 280 285 290	968
15	CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC TAC GTC AGC TTC CGT Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg 295 300 305	1016
20	GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala 310 315 320	1064
25	TAT TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC TCC TGT ATG AAC Tyr Tyr Cys Glu Gly Cys Ala Phe Pro Leu Asp Ser Cys Met Asn 325 330 335 340	1112
30	GCC ACC AAC CAT GCC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro 345 350 355	1160
35	GAT GTT GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GCC ACC Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr 360 365 370	1208
40	TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His 375 380 385	1256
45	CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCG CCCAGCATCC Arg Asn Met Val Val Lys Ala Cys Gly Cys His 390 395	1309
50	TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCTGCTA AAATTCTGGT CTTTCCCAGT TCCTCTGTCC TTCAATGGGT TTGGGGCTA TCACCCCCGCC CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC CTCAGCCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAAATTC TAAACTAGAT	1369 1429 1489 1549 1609 1669

5	GATCTGGGCT CTCTGCACCA TTCAATTGTGG CAGTTGGGAC ATTTTGTAGGT ATAACAGACA	1729
	CATAACACTTA GATCAATGCA TCGCTGTACT CCTTGAAATC AGAGCTAGCT TGTTAGAAAA	1789
	AGAATCAGAG CCAGGTATAG CGGTGCATGT CATTAAATCCC AGCGCTAAAG AGACAGAGAC	1849
10	AGGAGAAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAA	1909
	AAAAAAAAAAC CGAATTTC	1926

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 399 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- 20 (ix) FEATURE:
 - (D) OTHER INFORMATION: /product= "mOP2-PP"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

25	Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys	
	1 5 10 15	
	Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln	
	20 25 30	
30	Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala	
	35 40 45	
35	Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala	
	50 55 60 65	
	Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala	
	70 75 80	
40	Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg	
	85 90 95	
	Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr	
	100 105 110	
45	Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr	
	115 120 125 130	
	Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr	
	135 140 145	

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Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met
 150 155 160
 5 Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe
 165 170 175
 Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu
 180 185 190
 10 Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp
 195 200 205 210
 Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
 15 215 220 225
 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln
 230 235 240
 20 Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala
 245 250 255
 Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn
 260 265 270
 25 Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His
 275 280 285 290
 Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser
 30 295 300 305
 Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr
 310 315 320
 35 Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
 325 330 335
 Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
 340 345 350
 40 Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
 355 360 365 370
 Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
 45 375 380 385
 Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
 390 395
 50

(2) INFORMATION FOR SEQ ID NO:24:

5 (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1368
 (D) OTHER INFORMATION:/STANDARD NAME="60A"

20 (x) PUBLICATION INFORMATION:
 (A) AUTHORS: WHARTON, KRISTI A.; THOMSEN, GERALD H.;
 GELBERT, WILLIAM M.
 (B) TITLE: DROSOPHILA 60A GENE...
 (C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
 (D) VOLUME: 88
 (E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
 (F) PAGES: 9214-9218
 (G) DATE: OCT - 1991

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC	48
30	Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser	
	1 5 10 15	
	CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GCG ACC ACG CCG CCG	96
	Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	
35	20 25 30	
	GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC	144
	Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	
	35 40 45	
40	CAG ACG ATC ATG CAC AGA GTG CTG AGC GAG GAC GAC AAG CTG GAC GTC	192
	Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	
	50 55 60	
45	TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GCC GAA CGG CCG ACG CAC	240
	Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	
	65 70 75 80	
50	CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCC AAG TTC CTG	288
	Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	
	85 90 95	

	CTG GAC GTC TAC CAC CGC ATC ACG GCG GAG GAG GGT CTC AGC GAT CAG Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln 100 105 110	336
5	GAT GAG GAC GAC TAC GAA CGC GGC CAT CGG TCC AGG AGG AGC GCC Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala 115 120 125	384
10	GAC CTC GAG GAG GAT GAG GGC GAG CAG CAG AAG AAC TTC ATC ACC GAC Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp 130 135 140	432
15	CTG GAC AAG CGG GCC ATC GAC GAG AGC GAC ATC ATC ATG ACC TTC CTG Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu 145 150 155 160	480
20	AAC AAG CGC CAC CAC AAT GTG GAC GAA CTG CGT CAC GAG CAC GGC CGT Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg 165 170 175	528
	CGC CTG TGG TTC GAC GTC TCC AAC GTG CCC AAC GAC AAC TAC CTG GTG Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asn Tyr Leu Val 180 185 190	576
25	ATG GCC GAG CTG CGC ATC TAT CAG AAC GCC AAC GAG GGC AAG TGG CTG Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu 195 200 205	624
30	ACC GCC AAC AGG GAG TTC ACC ATC ACG GTA TAC GCC ATT GGC ACC GGC Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly 210 215 220	672
35	ACG CTG GGC CAG CAC ACC ATG GAG CCG CTG TCC TCG GTG AAC ACC ACC Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr 225 230 235 240	720
	GGG GAC TAC GTG GGC TGG TTG GAG CTC AAC GTG ACC GAG GGC CTG CAC Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His 245 250 255	768
40	GAG TGG CTG GTC AAG TCG AAG GAC AAT CAT GGC ATC TAC ATT GGA GCA Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala 260 265 270	816
45	CAC GCT GTC AAC CGA CCC GAC CGC GAG GTG AAG CTG GAC GAC ATT GGA His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly 275 280 285	864
50	CTG ATC CAC CGC AAG GTG GAC GAC GAG TTC CAG CCC TTC ATG ATC GGC Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly 290 295 300	912

	TTC TTC CGC GGA CCG GAG CTG ATC AAG GCG ACG GCC CAC AGC AGC CAC Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His 305 310 315 320	960
5	CAC AGG AGC AAG CGA AGC GCC AGC CAT CCA CGC AAG CGC AAG AAG TCG His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser 325 330 335	1008
10	G TG TCG CCC AAC AAC GTG CCG CTG CTG GAA CCG ATG GAG AGC ACG CGC Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg 340 345 350	1056
15	AGC TGC CAG ATG CAG ACC CTG TAC ATA GAC TTC AAG GAT CTG GGC TGG Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp 355 360 365	1104
20	CAT GAC TGG ATC ATC GCA CCA GAG GGC TAT GGC GCC TTC TAC TGC AGC His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser 370 375 380	1152
25	GGC GAG TGC AAT TTC CCG CTC AAT GCG CAC ATG AAC GCC ACG AAC CAT Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His 385 390 395 400	1200
30	GCG ATC GTC CAG ACC CTG GTC CAC CTG CTG GAG CCC AAG AAG GTG CCC Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro 405 410 415	1248
35	AAG CCC TGC TGC GCT CCG ACC AGG CTG GGA GCA CTA CCC GTT CTG TAC Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr 420 425 430	1296
40	CAC CTG AAC GAC GAG AAT GTG AAC CTG AAA AAG TAT AGA AAC ATG ATT His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile 435 440 445	1344
	GTG AAA TCC TGC GGG TGC CAT TGA Val Lys Ser Cys Gly Cys His 450 455	1368

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
 1 5 10 15

5 Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro
 20 25 30

Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp
 10 35 40 45

Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val
 50 55 60

15 Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His
 65 70 75 80

Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu
 85 90 95

20 Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln
 100 105 110

Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala
 25 115 120 125

Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp
 130 135 140

30 Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu
 145 150 155 160

Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg
 35 165 170 175

Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val
 180 185 190

40 Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu
 195 200 205

Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly
 45 210 215 220

Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr
 225 230 235 240

Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His
 50 245 250 255

Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala
 260 265 270

His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly
 275 280 285
 5 Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly
 290 295 300
 Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His
 305 310 315 320
 10 His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser
 325 330 335
 Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg
 340 345 350
 15 Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
 355 360 365
 20 His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
 370 375 380
 Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 385 390 395 400
 25 Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
 405 410 415
 Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
 420 425 430
 30 His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
 435 440 445
 35 Val Lys Ser Cys Gly Cys His
 450 455

(2) INFORMATION FOR SEQ ID NO:26:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

50 (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20 Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
1 5 10 15Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Try Cys Ser Gly
20 25 30Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
35 40 45Thr Ile Gln Ser Ile Val Ala Arg Ala Val Gly Val Val Pro Gly Ile
50 55 6030 Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
65 70 75 80Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
85 90 95Thr Val Glu Ser Cys Ala Cys Arg
100

40 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

5
 (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15

Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 20 25 30

15 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60

20 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80

25 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95

Arg Ser Cys Gly Cys His
 100

30 (2) INFORMATION FOR SEQ ID NO:28:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS

45 (ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15

Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30

5 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60

10 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80

Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Trp Met Val Val
 15 85 90 95

Arg Ala Cys Gly Cys His
 100

20 (2) INFORMATION FOR SEQ ID NO:29:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= OPX

35 /note- "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY
 SELECTED FROM THE RESIDUES OCCURRING AT THE
 CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE
 OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or
 16,18,20 and 22.)"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
 1 5 10 15

Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
 20 25 30

45 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
 35 40 45

Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
 50 55 60

50

55

Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
 65 70 75 80

5 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
 85 90 95

Xaa Ala Cys Gly Cys His
 100

10 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 5

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

25 Leu Xaa Xaa Xaa Phe

1 5

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

10

Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala

15 20

Xaa Tyr Cys Xaa Gly Xaa Cys Xaa

25 30

Xaa Pro Xaa Xaa Xaa Xaa Xaa

35

Xaa Xaa Xaa Asn His Ala Xaa Xaa

40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

55 60

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70 75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85 90

Xaa Cys Xaa Cys Xaa

95

50

55

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 6

10 (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
 1 5 10
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 15
 Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 20 25
 20 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 30 35
 Xaa Pro Xaa Xaa Xaa Xaa Xaa
 40
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 45 50
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 55
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 70
 30 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 85
 35 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Xaa Cys Xaa
 100

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 1238 base pairs, 372 amino acids
 (B) TYPE: nucleic acid, amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50

55

5

(iii) ORIGINAL SOURCE:
 (A) ORGANISM: human
 (P) TISSUE TYPE: BRAIN

10

(iv) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION:
 (D) OTHER INFORMATION:
 /product= "GDF-1"
 /note= "GDF-1 cDNA"

15

(x) PUBLICATION INFORMATION:
 (A) AUTHORS: Lee, Se-Jin
 (B) TITLE: Expression of Growth/Differentiation Factor 1
 (C) JOURNAL: Proc. Nat'l Acad. Sci.
 (D) VOLUME: 88
 (E) RELEVANT RESIDUES: 1-1238
 (F) PAGES: 4250-4254
 (G) DATE: May-1991

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGGGACACCG GCCCCGCCCT CAGCCCCTG GTCCCCGGCC GCCGGGACC CTGGCACTC	60
TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC Met Pro Pro Pro Gln Gln Gly Pro Cys Gly	113
1 5 10	
CAC CAC CTC CTC CTC CTG GCC CTG CTG CCC TCG CTG CCC His His Leu Leu Leu Leu Ala Leu Leu Pro Ser Leu Pro	158
15 20 25	
CTG ACC CGC GCC CCC GTG CCC CCA GGC CCA GCC GCC GCC CTG CTC Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu	203
30 35 40	
CAG GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCC CCC AGG CTC Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu	248
45 50 55	
CGG CCG GTT CCC CCG GTC ATG TGG CGC CTG TTT CGA CGC CGG GAC Arg Pro Val Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp	293
60 65 70	
CCC CAG GAG ACC AGG TCT GGC TCG CGG CGG ACG TCC CCA GGG GTC Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val	338
75 80 85	
ACC CTG CAA CCG TGC CAC GTG GAG GAG CTG GGG GTC GCC GGA AAC Thr Leu Gln Pro Cyc His Val Glu Glu Leu Gly Val Ala Gly Asn	383
90 95 100	

45

50

	ATC GTG CGC CAC ATC CCG GAC CGC GGT GCG CCC ACC CGG GCC TCG Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser 105 110 115	428
5	GAG CCT GTC TCG GCC GCG GGG CAT TGC CCT GAG TGG ACA GTC GTC Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val 120 125 130	473
10	TTC GAC CTG TCG GCT GTG GAA CCC GCT GAG CGC CCG AGC CGG GCC Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala 135 140 145	518
15	CGC CTG GAG CTG CGT TTC GCG GCG GCG GCG GCA GCC CCG GAG Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu 150 155 160	563
20	GCG GGC TGG GAG CTG AGC GTG GCG CAA GCG GGC CAG GGC GCG GGC Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly 165 170 175	608
25	GCG GAC CCC GGG CCG GTG CTG CTC CGC CAG TTG GTG CCC GCC CTG Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu 180 185 190	653
30	GGG CCG CCA GTG CGC GCG GAG CTG CTG GGC GCC GCT TGG GCT CGC Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg 195 200 205	698
35	AAC GCC TCA TGG CCG CGC AGC CTC CGC CTG GCG CTG GCG CTA CGC Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg 210 215 220	743
40	CCC CGG GCC CCT GCC TGC GCG CGC CTG GCC GAG GCC TCG CTG Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu 225 230 235	788
45	CTG CTG GTG ACC CTC GAC CCG CGC CTG TGC CAC CCC CTG GCC CGG Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg 240 245 250	833
50	CCG CGG CGC GAC GCC GAA CCC GTG TTG GGC GGC GGC CCC GGG GGC Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly 255 260 265	878
55	GCT TGT CGC CGG CGG CGG CTG TAC CTG AGC TTC CGC CAG GTG GGC Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly 270 275 280	923
60	TGG CAC CGC TGG GTC ATC GCG CCG CGC CCC TTC CTG GCC AAC TAC Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr 285 290 295	968

	TGC CAG GGT CAG TGC GCG CTG CCC GTC GCG CTG TCG GGG TCC GGG Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly 300 305 310	1013
5	GGG CCG CCG GCG CTC AAC CAC GCT GTG CTG CGC GCG CTC ATG CAC Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His 315 320 325	1058
10	GCG GCC GCC CCG GGA GCC GAC CTG CCC TGC TGC GTG CCC GCG Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala 330 335 340	1103
15	CGC CTG TCG CCC ATC TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn 345 350 355	1148
20	GTG GTG CTG CCG CAG TAT GAG GAC ATG GTG GTG GAC GAG TGC GGC Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly 360 365 370	1193
	TGC CGC TAACCCGGGG CGGGCAGGGA CCCGGCCCCA ACAATAAAATG CCGCGTGG Cys Arg 372	1238
25	(2) INFORMATION FOR SEQ ID NO:33:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 372 amino acids	
30	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
35	(iii) HYPOTHETICAL: NO	
	(iv) ANTI-SENSE: NO	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: human	
	(F) TISSUE TYPE: BRAIN	
	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
45	(B) LOCATION:	
	(D) OTHER INFORMATION: /function=	
	/product= "GDF-1"	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	

Met Pro Pro Pro Gln Gln Gly Pro Cys Gly
1 5 10

	His His Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro	
	15 20 25	
5	Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu	
	30 35 40	
	Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu	
	45 50 55	
10	Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp	
	60 65 70	
15	Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val	
	75 80 85	
	Thr Leu Gln Pro Cyc His Val Glu Glu Leu Gly Val Ala Gly Asn	
	90 95 100	
20	Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser	
	105 110 115	
	Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val	
	120 125 130	
25	Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala	
	135 140 145	
30	Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu	
	150 155 160	
	Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly	
	165 170 175	
35	Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu	
	180 185 190	
	Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg	
	195 200 205	
40	Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg	
	210 215 220	
45	Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu	
	225 230 235	
	Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg	
	240 245 250	
50	Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly	
	255 260 265	

	Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly		
	270	275	280
5	Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr		
	285	290	295
	Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly		
10	300	305	310
	Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His		
	315	320	325
15	Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala		
	330	335	340
	Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn		
	345	350	355
20	Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly		
	360	365	370
	Cys Arg		
25	372		

30 **Claims**

1. Use of a morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal (eg a human) and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises a sequence sharing at least 70% amino acid sequence homology with the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq. ID No. 5), for the manufacture of a medicament for:
 - (a) modulating an inflammatory response; or
 - (b) alleviating the tissue destructive effects associated with the inflammatory response to tissue injury; or
 - (c) enhancing the viability of injured or damaged mammalian tissue (eg tissue disposed *in vivo* in a mammal).
2. Use according to claim 1 for modulating an inflammatory response in mammalian tissue, wherein the modulation of said inflammatory response comprises:
 - (a) alleviation of fibrosis or scar tissue formation; and/or
 - (b) inhibition of adherence of immune effector cells to vascular endothelium; and/or
 - (c) alleviation of interstitial inflammation; and/or
 - (d) alleviation of edema or erythema; and/or
 - (e) alleviation of inflammatory tissue necrosis.
3. Use according to claim 1 or claim 2 wherein the inflammatory response is associated with tissue injury (the injury for example being chemically, mechanically, biologically or immunologically related).
4. Use according to any one of the preceding claims wherein said medicament is administered: (a) for the treatment or prophylaxis of said tissue injury; and/or (b) in an amount effective to inhibit fibrogenesis or stimulate tissue-specific regeneration of said injured or damaged tissue; and/or (c) to inhibit loss or reduction of function of said tissue; and/or (d) orally, parenterally or topically; and/or (e) dispersed in a liquid tissue adhesive; and/or (f) in an aerosol.
5. Use according to claim 3 or 4 wherein said tissue injury includes:

- (a) ischaemic-reperfusion injury; or
- (b) hyperoxia injury.

6. Use according to claim 5(a) wherein said ischaemic-reperfusion injury is:

- 5 (a) associated with cardiac arrest, pulmonary occlusion, arterial (eg renal artery) occlusion, coronary occlusion or occlusive stroke; or
- (b) associated with surgery or the reduction or interruption of blood flow to an organ in a clinical procedure (eg carotid endarterectomy, coronary artery bypass, a tissue grafting procedure, an organ transplant or fibrinolytic therapy); or
- 10 (c) associated with cerebral infarction, myocardial infarction, asphyxia or cardiopulmonary arrest.

7. Use according to claim 5(b) wherein the hyperoxia injury is associated with the treatment of:

- 15 (a) a prematurely newborn baby; or
- (b) emphysema; or
- (c) asphyxia.

8. Use according to any one of the preceding claims wherein the tissue is lung, cardiac, hepatic, neural, pancreatic, synovial, skin or renal tissue, for example wherein:

- 20 (a) the tissue is renal tissue and the mammal is afflicted with glomerular nephritis, atherosclerosis or diabetes, or
- (b) the tissue is cardiac tissue and the mammal is afflicted with atherosclerosis or vascular disease, or
- 25 (c) the tissue is pancreatic tissue and the mammal is afflicted with diabetes, or
- (d) the tissue is synovial tissue and the mammal is afflicted with arthritis,
- (e) the tissue is skin tissue and the mammal is afflicted with dermatitis or psoriasis,
- (f) the tissue is lung tissue and the mammal is afflicted with bronchitis, emphysema, idiopathic pulmonary fibrosis, asthma, asphyxia, or adult respiratory distress syndrome.

30 9. Use according to claim 3 or 4 wherein the tissue injury includes:

- 35 (a) an immune-cell mediated inflammatory response; or
- (b) an inflammatory disease (eg a chronic inflammatory disease); or
- (c) an abnormal immune response; or
- (d) edema or erythema.

10. Use according to claim 9(a), 9(c) or 9(d) wherein the tissue injury includes:

- 40 (a) a generalized acute inflammatory response; or
- (b) airway inflammation.

11. Use according to claim 9(b) wherein the inflammatory disease includes:

- 45 (a) an autoimmune disease; or
- (b) arthritis, psoriasis, dermatitis, inflammatory bowel disease or diabetes.

12. Use according to claim 10 wherein:

- 50 (a) in claim 10(a) the acute inflammatory response is associated with asphyxia or adult respiratory distress syndrome; or
- (b) in claim 10(b) the airway inflammation is associated with chronic bronchitis, emphysema, idiopathic pulmonary fibrosis or asthma.

55 13. Use according to claim 11 wherein:

- (a) in claim 11(a) the autoimmune disease is a neurodegenerative disease (eg multiple sclerosis or amyotrophic lateral sclerosis); or

(b) in claim 11(b) the arthritis is rheumatoid, degenerative or psoriatic arthritis.

14. Use according to any one of claims 3-13 wherein the modulation of the inflammatory response is effected by administration of the medicament before or after the injury, for example prior to or after the reduction or interruption of blood flow or after resumption of blood flow when the injury is ischaemic-reperfusion injury.
- 5 15. Use according to claim 6(b) wherein said clinical procedure is a tissue grafting procedure (eg of skin, bone marrow or gastrointestinal mucosa tissue) or an organ transplant procedure (eg of lung, heart, kidney, liver or pancreas).
- 10 16. Use according to claim 15 wherein the modulation of the inflammatory response is effected by administration of the medicament:
 - (a) upon or following removal of the organ or tissue from a donor host; or
 - (b) during storage or transportation of the organ or tissue prior to implantation into a recipient host; or
 - 15 (c) upon or following implantation into a recipient host.
17. Use according to any one of the preceding claims wherein said medicament comprises the morphogen dispersed in a physiologically acceptable aqueous carrier suitable for parenteral administration to a mammal.
- 20 18. Use according to any one of the preceding claims wherein the amino acid sequence of said polypeptides comprises a sequence that:
 - (a) shares at least 80% homology with the sequence of said seven cysteine domain of human OP-1; or
 - (b) shares at least 60% amino acid identity, eg at least 65% identity, with the sequence of said seven cysteine domain of human OP-1; or
 - 25 (c) comprises the sequence of the seven cysteine domain of human OP-1, mouse OP-1, human OP-2, mouse OP-2 or 60A, or naturally occurring or biosynthetic variant of any thereof, provided that any said variant induces tissue specific morphogenesis in said mammal; or
 - (d) comprises an amino acid sequence selected from Seq. ID Nos 9, 10, 11, 12, 13, 14, 26, 27, 28 or 29 (CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx), GDF-1(fx), BMP3, BMP5, BMP6 or OPX) or a naturally occurring or biosynthetic variant of any thereof, provided that any said variant induces tissue-specific morphogenesis in said mammal, or
 - 30 (e) comprises an amino acid sequence of residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8 or residues 354-455 of Seq ID No. 24, or a naturally occurring or biosynthetic variant of any thereof, provided that any said variant induces tissue-specific morphogenesis in said mammal.
 - 35 19. A pharmaceutical composition for use in alleviating injury associated with exposure of mammalian tissue to toxic oxygen concentrations, comprising a morphogen dispersed in a physiologically acceptable aqueous carrier to a concentration effective for alleviating extravasation of immune effector cells, interstitial inflammation, edema, necrosis or fibrogenesis in mammalian tissue at risk of, or afflicted with, said injury, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises a sequence sharing at least 70% amino acid sequence homology with the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq. ID No. 5), said composition further comprising a free oxygen radical inhibiting agent or an anticoagulant.
 - 40 20. A pharmaceutical composition for topical administration to mammalian epithelial tissue, comprising a morphogen dispersed in a dermatologically acceptable carrier or in a biocompatible, non-irritating tissue surface adhesive (eg hydroxypropylcellulose) to a concentration effective for alleviating extravasation of immune effector cells, interstitial inflammation, edema, necrosis or fibrogenesis in mammalian tissue at risk of, or afflicted with, said injury, said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises a sequence sharing at least 70% amino acid sequence homology with the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq ID No. 5).
 - 45 21. A preservation solution for maintaining *ex vivo* viability of mammalian cells or tissue or a mammalian organ, comprising a fluid formulation having an osmotic pressure substantially equivalent to the osmotic pressure of living mammalian cells and a morphogen dispersed in said fluid to a concentration effective for alleviating extravasation of immune effector cells, interstitial inflammation, edema, necrosis or fibrogenesis in said cells, tissue or organ,

said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises a sequence sharing at least 70% amino acid sequence homology with the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq. ID No. 5).

5 **22.** A solution according to claim 21, further comprising a sugar, an anticoagulant or a free oxygen radical inhibiting agent; or, further formulated to maintain substantially normal ATP levels in said cells, tissue or organ.

10 **23.** The composition of claim 19 or 20 or the solution of claim 21 or 22 wherein the morphogen is as defined in claim 18.

15 **24.** An ex vivo method for protecting a living mammalian tissue or transplanted mammalian organ from injury associated with the inflammatory response of activated immune effector cells comprising the step of providing to said tissue or organ a morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises a sequence sharing at least 70% amino acid sequence homology with the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq. ID No. 5).

20 **25.** The method of claim 24 wherein:

- (a) the tissue or organ is as defined in claim 15; and/or
- (b) the morphogen is as defined in claim 18;
- (c) the morphogen is provided in the form of a solution as defined in claim 21 or 22.

Patentansprüche

25 **1.** Verwendung eines Morphogens, das ein dimeres Protein umfaßt, das bei einem Säugetier (beispielsweise einem Menschen) eine gewebsspezifische Morphogenese induziert und zwei gefaltete Polypeptide umfaßt, wobei die Aminosäure-Sequenz von jedem eine Sequenz umfaßt, die zumindest 70% Aminosäure-Sequenz-Homologie mit der C-terminalen Sieben-Cystein-Domäne von menschlichem OP-1 teilt (Reste 38-139 von Seq. ID Nr. 5), zur Herstellung eines Medikamentes zur:

- (a) Modulierung einer Entzündungsreaktion; oder
- (b) Verminderung der Gewebs-zerstörenden Wirkungen, die mit der Entzündungsreaktion auf eine Gewebs-schädigung verbunden sind; oder
- (c) Steigerung der Lebensfähigkeit von verletztem oder geschädigtem Säugetiergegewebe (beispielsweise Gewebe, das sich *in vivo* in einem Säugetier befindet).

30 **2.** Verwendung nach Anspruch 1 zur Modulierung einer Entzündungsreaktion in Säugetiergegewebe, wobei die Modu-lation der Entzündungreaktion folgendes umfaßt:

- (a) Verminderung einer Fibrose oder Narbengewebsbildung; und/oder
- (b) Hemmung der Anhaftung von Immuneffektorzellen an vaskuläres Endothel; und/oder
- (c) Verminderung einer interstitiellen Entzündung; und/oder
- (d) Verminderung eines Ödems oder Erythems; und/oder
- (e) Verminderung einer entzündlichen Gewebsnekrose.

35 **3.** Verwendung nach Anspruch 1 oder Anspruch 2, bei der die Entzündungsreaktion mit einer Gewebs-schädigung verbunden ist (wobei die Verletzung beispielsweise chemisch, mechanisch, biologisch oder immunologisch verur-sacht ist).

40 **4.** Verwendung nach einem der vorhergehenden Ansprüche, bei der das Medikament:

(a) zur Behandlung oder Prophylaxe der Gewebsschädigung; und/oder

(b) in einer Menge, die zur Hemmung einer Fibrogenese oder zur Stimulierung einer gewebsspezifischen Regeneration des verletzten oder geschädigten Gewebes wirksam ist; und/oder

5 (c) zur Hemmung eines Verlustes oder einer Verminderung der Funktion des Gewebes; und/oder

(d) oral, parenteral oder topisch; und/oder

10 (e) in einem flüssigen Gewebsklebstoff dispergiert; und/oder

(f) in einem Aerosol verabreicht wird.

15 5. Verwendung nach Anspruch 3 oder Anspruch 4, bei der die Gewebsschädigung:

(a) eine ischämische Reperfusions-Schädigung; oder

(b) Hyperoxie-Schädigung

20 einschließt.

6. Verwendung gemäß Anspruch 5 (a), bei der die ischämische Reperfusions- Schädigung:

(a) mit Herzstillstand, Lungenarterienverschluß, Arterienverschluß (beispielsweise Nierenarterienverschluß), Koronararterienverschluß oder durch Okklusion verursachten Schlag verbunden ist; oder

25 (b) mit einem chirurgischen Eingriff oder der Verminderung oder Unterbrechung des Blutstromes zu einem Organ bei einem klinischen Verfahren (beispielsweise einer Carotis-Enterektomie, aorto-koronarem Bypass, einem Gewebstransplantationsverfahren, einer Organtransplantations- oder fibronolytische Therapie) verbunden ist; oder

30 (c) mit einem Gehirninfarkt, Herzinfarkt, mit Asphyxie oder Herz-/Lungenstillstand verbunden ist.

7. Verwendung nach Anspruch 5 (b), bei der die Hyperoxie-Schädigung mit der Behandlung:

35 (a) eines frühgeborenen Säugling; oder

(b) Emphysems; oder

(c) Asphyxie

40 verbunden ist.

8. Verwendung nach einem der vorhergehenden Ansprüche, bei der das Gewebe Lungen-, Herz-, Leber-, Nerven-, Pankreas-, Synovial-, Haut- oder Nierengewebe ist, bei dem beispielsweise:

45 (a) das Gewebe Nierengewebe ist und das Säugetier an glomerulärer Nephritis, Arteriosklerose oder Diabetes leidet, oder

(b) das Gewebe Herzgewebe ist und das Säugetier an Arteriosklerose oder einer Gefäßerkrankung leidet, oder

50 (c) das Gewebe Pankreasgewebe ist und das Säugetier an Diabetes leidet, oder

(d) das Gewebe Synovialgewebe ist und das Säugetier an Arthritis leidet,

55 (e) das Gewebe Hautgewebe ist und das Säugetier an Dermatitis oder Psoriasis leidet,

(f) das Gewebe Lungengewebe ist und das Säugetier an Bronchitis, Emphysem, ideopathischer Lungenfi-

brose, Asthma, Asphyxie oder Schocklunge leidet.

9. Verwendung nach Anspruch 3 oder Anspruch 4, bei der die Gewebsverletzung:

5 (a) eine Immunzell-vermittelte Entzündungsreaktion; oder
 (b) eine entzündliche Erkrankung (beispielsweise eine chronische entzündliche Erkrankung); oder
 (c) eine abnormale Immunreaktion; oder
10 (d) ein Ödem oder Erythem
 einschließt.

10. Verwendung nach Anspruch 9 (a), 9 (c) oder 9 (d), bei der die Gewebsschädigung:

15 (a) eine generalisierte akute entzündliche Reaktion; oder
 (b) Atemwegsentzündung
 einschließt.

20 11. Verwendung nach Anspruch 9 (b), bei der die entzündliche Erkrankung:
 (a) eine Autoimmunerkrankung; oder
 (b) Arthritis, Psoriasis, Dermatitis, eine entzündliche Darmerkrankung oder Diabetes
25 einschließt.

12. Verwendung nach Anspruch 10, bei der:
 (a) in Anspruch 10 (a) die akute entzündliche Reaktion mit Asphyxie oder Schocklunge verbunden ist; oder
30 (b) in Anspruch 10 (b) die Atemwegsentzündung mit chronischer Bronchitis, Emphysem, ideopathischer Lungenfibrose oder Asthma verbunden ist.

13. Verwendung nach Anspruch 11, bei der:
35 (a) in Anspruch 11 (a) die Autoimmunerkrankung eine neurodegenerative Erkrankung (beispielsweise Multiple Sklerose oder amyotrophe Lateralsklerose) ist; oder
 (b) in Anspruch 11 (b) die Arthritis eine rheumatoide, degenerative oder psoriatische Arthritis ist.

40 14. Verwendung nach einem der Ansprüche 3 bis 13, bei der die Modulation der Entzündungsreaktion durch Verabreichung des Medikaments vor oder nach der Schädigung, beispielsweise vor oder nach der Verringerung oder Unterbrechung des Blutstromes oder nach Wiederaufnahme eines Blutstromes verabreicht wird, wenn die Schädigung eine ischämische Reperfusions-Schädigung ist.

45 15. Verwendung nach Anspruch 6 (b), bei der das klinische Verfahren ein Gewebs-Transplantations-Verfahren (beispielsweise von Haut-, Knochenmark- oder Gewebe der Gastrointestinalschleimhaut) oder ein Organtransplantations-Verfahren (beispielsweise von Lunge, Herz, Niere, Leber oder Pankreas) ist.

50 16. Verwendung nach Anspruch 15, bei der die Modulation der Entzündungsreaktion durch Verabreichung des Medikamentes:
 (a) bei oder im Anschluß an die Entfernung des Organs oder Gewebes von einem Spender; oder
 (b) während der Aufbewahrung oder des Transportes des Organs oder Gewebes vor Implantation in einen Empfänger; oder
55 (c) bei oder im Anschluß an Implantation in einen Empfänger
 bewirkt wird.

17. Verwendung nach einem der vorhergehenden Ansprüche, bei der das Medikament das das Morphogen in einem physiologisch akzeptablen wässrigen Träger, der zur parenteralen Verabreichung an ein Säugetier geeignet ist, dispergiert umfaßt.

5 18. Verwendung nach einem der vorhergehenden Ansprüche, bei der die Aminosäure-Sequenz des Polypeptides eine Sequenz umfaßt, die:

(a) zumindest 80% Homologie mit der Sequenz der Sieben-Cystein-Domäne von menschlichem OP-1 teilt; oder

10 (b) zumindest 60% Aminosäure-Identität, beispielsweise zumindest 65% Identität, mit der Sequenz der Sieben-Cystein-Domäne von menschlichem OP-1 teilt; oder

15 (c) die Sequenz der Sieben-Cystein-Domäne von menschlichem OP-1, Maus OP-1, menschlichem OP-2, Maus OP-2 oder 60A oder deren natürlich vorkommende oder biosynthetische Varianten umfaßt, vorausgesetzt, daß irgendeine dieser Varianten eine gewebsspezifische Morphogenese bei dem Säugetier induziert; oder

20 (d) eine Aminosäure-Sequenz umfaßt, die aus den Sequenz ID Nr. 9, 10, 11, 12, 13, 14, 26, 27, 28 oder 29 (CBMP2A (fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx), GDF-1(fx), BMP3, BMP5, BMP6 oder OPX) oder einer natürlich vorkommenden oder biosynthetischen Variante davon ausgewählt ist, vorausgesetzt, daß jede dieser Varianten eine gewebsspezifische Morphogenese bei dem Säugetier induziert, oder

25 (e) eine Aminosäure-Sequenz der Reste 38-139 von Sequenz ID Nr. 5, 6, 7 oder 8 oder der Reste 354-455 von Sequenz ID Nr. 24 oder eine natürlich vorkommende oder biosynthetische Variante von irgendeiner davon umfaßt, vorausgesetzt, daß jede der Varianten eine gewebsspezifische Morphogenese bei dem Säugetier induziert.

30 19. Pharmazeutische Zusammensetzung zur Verwendung bei der Linderung einer Verletzung, die mit der Exposition von Säugetiergebebe gegenüber toxischen Sauerstoff-Konzentrationen verbunden ist, die ein Morphogen in einem physiologisch verträglichen wässrigen Träger in einer Konzentration dispergiert umfaßt, die zur Verminderung einer Extravasation von Immuneffektorzellen, einer interstitiellen Entzündung, eines Ödems, einer Nekrose oder einer Fibrogenese in Säugetiergebebe wirksam ist, das dem Risiko der Schädigung ausgesetzt ist oder darunter leidet, wobei das Morphogen ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz jedes der beiden eine Sequenz umfaßt, die zumindest 70% Aminosäure-Sequenz-Homologie mit der C-terminalen Sieben-Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) umfaßt, wobei die Zusammensetzung weiterhin ein Mittel zur Hemmung freier Sauerstoff-Radikale oder ein Antikoagulanztumfaßt.

35 40 20. Pharmazeutische Zusammensetzung zur topischen Verabreichung an Säugetier-Epitelgewebe, die ein in einem dermatologisch akzeptablen Träger oder in einem biokompatiblen, nicht reizenden Geweboberflächenklebstoff (z.B. Hydroxypropyl-zellulose) in einer Konzentration dispergiert umfaßt, die zur Verminderung der Extravasation von Immuneffektorzellen, einer interstitiellen Entzündung, eines Ödems, einer Nekrose oder Fibrogenese bei Säugetiergebebe wirksam ist, das dem Risiko Schädigung ausgesetzt ist oder darunter leidet, wobei das Morphogen ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz jedes der beiden eine Sequenz umfaßt, die zumindest 70% Aminosäure-Sequenz-Homologie mit der C-terminalen Sieben-Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) teilt.

45 50 21. Eine Konservierungslösung zur Aufrechterhaltung der *ex vivo* -Lebensfähigkeit von Säugetierzellen oder -gewebe oder eines Säugetierorgans, das eine flüssige Zubereitung umfaßt, die einen im wesentlichen dem osmotischen Druck lebender Säugetierzellen äquivalenten Druck und ein in der Flüssigkeit in einer Konzentration dispergiertes Morphogen aufweist, die zur Verminderung der Extravasation von Immuneffektorzellen, einer interstitiellen Entzündung, eines Ödems, einer Nekrose oder Fibrogenese bei diesen Zellen, Gewebe oder Organ wirksam ist, wobei das Morphogen ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz von jedem eine Sequenz umfaßt, die zumindest 70% Aminosäure-Sequenz-Homologie mit der C-terminalen Sieben-

Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) teilt.

- 22. Lösung nach Anspruch 21, die weiterhin einen Zucker, ein Antikoagulanz oder ein Mittel zur Hemmung freier Sauerstoff-Radikale umfaßt; oder weiterhin zur Aufrechterhaltung von im wesentlichen normalen ATP-Spiegeln in diesen Zellen, Gewebe oder Organ formuliert ist.
- 5 23. Zusammensetzung nach Anspruch 19 oder Anspruch 20 oder die Lösung nach Anspruch 21 oder 22, bei der das Morphogen wie in Anspruch 18 definiert ist.
- 10 24. Ex-vivo-Verfahren zum Schutz eines lebenden Säugetiergebutes oder transplantierten Säugetierorganes vor einer Schädigung, die mit der Entzündungsreaktion von aktivierten Immuneffektorzellen verbunden ist, das den Schritt umfaßt, dem Gewebe oder Organ ein Morphogen zu verabreichen, das ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz von jedem eine Sequenz umfaßt, die zumindest 70% Aminosäure-Sequenz-Homologie mit der C-terminalen Sieben-Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) teilt.
- 15 25. Verfahren nach Anspruch 24, bei dem:
 - 20 (a) das Gewebe oder Organ wie in Anspruch 15 definiert ist; und/oder
 - (b) das Morphogen wie in Anspruch 18 definiert ist; und/oder
 - (c) das Morphogen in der Form einer Lösung wie in Anspruch 21 oder 22 definiert verabreicht wird.

25 Revendications

- 1. Utilisation d'un morphogène comprenant une protéine dimérique qui induit la morphogenèse tissu-spécifique chez un mammifère (par exemple un humain) et comprend une paire de polypeptides repliés, la séquence des acides aminés de chacun de ceux-ci comprend une séquence partageant au moins 70% d'homologie de séquence des acides aminés avec le domaine à sept cystéines du C-terminal de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5), pour la fabrication d'un médicament pour :
 - 30 (a) moduler une réponse inflammatoire; ou
 - (b) ralentir les effets de détérioration tissulaire associés à la réponse inflammatoire provoquée par une lésion tissulaire; ou
 - (c) accroître la viabilité des tissus lésés ou endommagés de mammifère (par exemple un tissu placé in vivo dans un mammifère).
- 2. Utilisation selon la revendication 1 pour moduler une réponse inflammatoire dans un tissu de mammifère, dans laquelle la modulation de cette réponse inflammatoire comprend:
 - 35 (a) Le ralentissement de la formation des tissus fibrosés ou cicatriciels; et/ou
 - (b) l'inhibition de l'adhérence des cellules effectrices immunes sur l'endothélium vasculaire; et/ou
 - (c) le ralentissement d'une inflammation interstitielle; et/ou
 - (d) le ralentissement d'un oedème ou érythème; et/ou
 - (e) le ralentissement d'une nécrose des tissus inflammatoires.
- 3. Utilisation selon la revendication 1 ou la revendication 2 d'après laquelle la réponse inflammatoire est associée à une lésion tissulaire (la lésion étant par exemple liée à des causes chimiques, mécaniques, biologiques ou immunologiques).
- 4. Utilisation selon l'une quelconque des revendications précédentes dans laquelle ledit médicament est administré :
 - 45 (a) pour le traitement ou la prophylaxie de ladite lésion tissulaire; et/ou (b) en une quantité efficace pour inhiber la fibrogénèse ou stimuler la régénération tissu-spécifique de ce tissu lésé ou endommagé; et/ou (c) pour inhibiter la perte ou la diminution de la fonction dudit tissu ;et/ou (d) par voie orale, parentérale ou topique; et/ou (e) dispersé

dans un adhésif liquide tissulaire; et/ou (f) dans un aérosol.

5. Utilisation selon la revendication 3 ou 4 dans laquelle la dite lésion tissulaire comporte:

5 (a) une lésion ischémique par reperfusion; ou
 (b) une lésion par hyperoxie.

6. Utilisation selon la revendication 5(a) dans laquelle la dite lésion ischémique par reperfusion est:

10 (a) associée à un arrêt cardiaque, une occlusion pulmonaire, une occlusion artérielle (par exemple d'une artère rénale), une occlusion d'une artère coronaire ou une attaque à caractère occlusif; ou
 (b) associée à la chirurgie ou à la diminution ou à l'interruption de la circulation du sang vers un organe dans un traitement clinique (par exemple entérectomie de la carotide, un pontage d'une artère coronaire, un procédé de greffage d'un tissu, une transplantation d'organe ou une thérapie fibrinolytique); ou
15 (c) associée à un infarctus cérébral, un infarctus du myocarde, une asphyxie ou un arrêt cardio-pulmonaire.

7. Utilisation selon la revendication 5(b) dans laquelle la lésion à caractère hyperoxie est associée au traitement :

20 (a) d'un nouveau-né prématuré; ou
 (b) d'un emphysème; ou
 (c) d'une asphyxie.

8. Utilisation selon l'une quelconque des revendications précédentes d'après laquelle le tissu est un tissu pulmonaire, cardiaque, hépatique, neural, pancréatique, synovial, de la peau ou rénal, par exemple dans lequel:

25 (a) le tissu est un tissu rénal et le mammifère souffre d'une néphrite glomérulaire, d'athérosclérose ou d'un diabète, ou
 (b) le tissu est un tissu cardiaque et le mammifère souffre d'une athérosclérose ou d'une maladie vasculaire, ou
30 (c) le tissu est un tissu pancréatique et le mammifère souffre du diabète, ou
 (d) le tissu est un tissu synovial et le mammifère souffre d'arthrite,
 (e) le tissu est un tissu de la peau et le mammifère souffre d'une dermatite ou d'un psoriasis,
 (f) le tissu est un tissu du poumon et le mammifère souffre d'une bronchite, d'emphysème, de fibrose pulmo-
 naire protopathique, d'asthme, d'asphyxie, ou du syndrome d'une douleur respiratoire de l'adulte.

35 9. Utilisation selon la revendication 3 ou 4 dans laquelle la lésion tissulaire comporte :

40 (a) une réponse inflammatoire à médiation de cellules immunitaires;
 (b) une maladie inflammatoire (par exemple une maladie inflammatoire chronique); ou
 (c) une réponse immunitaire anormale; ou
 (d) un oedème ou un érythème.

10. Utilisation selon la revendication 9(a), 9(c), ou 9(d) dans laquelle la lésion tissulaire comporte:

45 (a) une réponse inflammatoire aiguë généralisée; ou
 (b) une inflammation des voies aériennes.

11. Utilisation selon la revendication 9(b) d'après laquelle la maladie inflammatoire comporte :

50 (a) une maladie auto-immune; ou
 (b) l'arthrite, un psoriasis, une dermatite, une maladie d'inflammation des intestins ou un diabète.

12. Utilisation selon la revendication 10 dans laquelle :

55 (a) dans la revendication 10(a) la réponse inflammatoire aiguë est associée à une asphyxie ou à un syndrome d'une douleur respiratoire de l'adulte; ou
 (b) dans la revendication 10(b) l'inflammation de la voie aérienne est associée à une bronchite chronique, un emphysème, une fibrose pulmonaire protopathique ou à de l'asthme.

13. Utilisation selon la revendication 11 dans laquelle:

- (a) dans la revendication 11(a) la maladie auto-immune est une maladie neuro-dégénérative (par exemple une sclérose multiple ou une sclérose latérale amyotrophique); ou
- 5 (b) dans la revendication 11(b) l'arthrite est à caractère rhumatismal, dégénératif ou arthrite psoriasique.

14. Utilisation selon l'une quelconque des revendications 3-13 dans laquelle la modulation de la réponse inflammatoire est effectuée par l'administration d'un médicament avant ou après la lésion, par exemple avant ou après la réduction ou l'interruption de la circulation du sang ou après la reprise de la circulation du sang lorsque la lésion est une lésion ischémique par reperfusion.

15. Utilisation selon la revendication 6(b) dans laquelle la dite procédure clinique est un procédé de greffage d'un tissu (par exemple de peau, de moelle osseuse ou d'un tissu de la muqueuse gastro-intestinale) ou un procédé de transplantation d'un organe (par exemple d'un poumon, d'un cœur, d'un rein, d'un foie ou d'un pancréas).

16. Utilisation selon la revendication 15 d'après laquelle la modulation de la réponse inflammatoire est effectuée par l'administration du médicament:

- (a) dès ou après l'élimination de l'organe ou du tissu provenant d'un hôte donneur; ou
- 20 (b) pendant la conservation ou le transport de l'organe ou du tissu avant l'implantation chez un hôte receveur; ou
- (c) dès ou après l'implantation chez l'hôte receveur.

17. Utilisation selon l'une quelconque des revendications précédentes d'après laquelle ledit médicament comprend le morphogène dispersé dans un véhicule aqueux approprié physiologiquement acceptable pour une administration par voie parentérale à un mammifère.

18. Utilisation selon l'une quelconque des revendications précédentes dans laquelle la séquence des acides aminés desdits polypeptides comprend une séquence qui:

- (a) partage au moins 80% d'homologie avec la séquence dudit domaine à sept cystéines de l'OP-1 humaine; ou
- 30 (b) partage au moins 60% d'identité des acides aminés, par exemple au moins 65 % d'identité, avec la séquence dudit domaine à sept cystéines de l'OP-1 humaine; ou
- (c) comprend la séquence du domaine à sept cystéines de l'OP-1 humaine, OP-1 de souris, OP-2 humaine, OP-2 ou 60A de souris, ou une variante naturelle ou biosynthétique de chacun de ceux-ci, pourvu que chacune de ces variantes induise une morphogenèse tissu-spécifique chez ledit mammifère; ou
- 35 (d) comprend une séquence d'acides aminés choisie parmi la séquence ID Nos. 9, 10, 11, 12, 13, 14, 26, 27, 28 ou 29 (CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgr1(fx), GDF-1(fx), BMP3, BMP5, BMP6 ou OPX) ou une variante naturelle ou biosynthétique de chacune de celles-ci, pourvu qu'une quelque variante induise une morphogenèse tissu-spécifique dans ledit mammifère; ou
- 40 (e) comprend une séquence des acides aminés des résidus 38-139 de la séquence ID No. 5, 6, 7 ou 8 ou les résidus 354-455 de la séquence ID No. 24, ou une variante naturelle ou biosynthétique de chacune de celles-ci, pourvu qu'une quelque variante de ces variantes induise une morphogenèse tissu-spécifique chez le dit mammifère.

45 19. Une composition pharmaceutique pour l'utilisation dans le ralentissement des lésions associées à une exposition d'un tissu d'un mammifère à des concentrations toxiques d'oxygène, comprenant un morphogène dispersé dans un véhicule aqueux physiologiquement acceptable à une concentration efficace pour ralentir l'extravasation des cellules effectrices immunes, un inflammation interstitielle, un oedème, une nécrose ou fibrogenèses dans un tissu de mammifère à risque, ou ayant souffert de, cette lésion, ledit morphogène comprenant une protéine dimérique qui induit une morphogenèse tissu-spécifique chez un mammifère, cette protéine dimérique comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celles-ci comprend une séquence partageant au moins 70% d'homologie de la séquence des acides aminés avec le domaine à sept cystéines du C-terminal de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5), la dite composition comprenant en outre un agent inhibant ou un anticoagulant à radical oxygène libre.

50 20. Une composition pharmaceutique pour une administration topique à un tissu épithelial de mammifère, comprenant

un morphogène dispersé dans un véhicule dermatologiquement acceptable ou dans l'adhésif d'une surface d'un tissu biocompatible, non irritant (par exemple l'hydroxypropylcellulose) à une concentration efficace pour ralentir l'extravasation des cellules effectrices immunes, d'une inflammation interstitielle, d'un oedème, d'une nécrose ou fibrogenèse dans un tissu de mammifère à risque de, ou ayant souffert de la dite lésion, ledit morphogène comprenant une protéine dimérique qui induit une morphogenèse tissu-spécifique chez un mammifère, ladite protéine dimérique comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celles-ci comprend une séquence partageant au moins 70% d'homologie de la séquence des acides aminés avec le domaine à sept cystéines du C-terminal de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5).

5 **21.** Une solution de conservation pour maintenir la viabilité ex vivo de cellules ou d'un tissu d'un mammifère ou d'un organe d'un mammifère, comprenant une formulation liquide possédant une pression osmotique essentiellement équivalente à la pression osmotique des cellules vivantes de mammifère et un morphogène dispersé dans ce liquide à une concentration efficace pour ralentir l'extravasation des cellules effectrices immunes, une inflammation interstitielle, un oedème, une nécrose ou fibrogenèse dans ces cellules , tissu ou organe, ledit morphogène comprenant une protéine dimérique qui induit une morphogenèse tissu-spécifique chez un mammifère, ladite protéine dimérique comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celles-ci comprend une séquence partageant au moins 70% d'homologie de la séquence des acides aminés avec le C-terminal du domaine à sept cystéine de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5).

10 **22.** Une solution selon la revendication 21, comprenant en outre un sucre, un anticoagulant ou un agent inhibant à radical oxygène libre; ou, en outre formulé pour essentiellement maintenir les niveaux normaux d'ATP dans lesdites cellules, tissu ou organe.

15 **23.** Une composition selon la revendication 19 ou 20 ou la solution selon la revendication 21 ou 22 dans laquelle le morphogène est tel que défini dans la revendication 18.

20 **24.** Une méthode ex vivo pour protéger un tissu vivant de mammifère ou un organe transplanté de mammifère contre des lésions associées à une réponse inflammatoire de cellules effectrices immunes activées comprenant l'étape de fournir au dit tissus ou organe un morphogène comprenant une protéine dimérique qui induit une morphogenèse tissu-spécifique chez un mammifère, la dite protéine dimérique comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celle-ci comprend une séquence partageant au moins 70% d'homologie de la séquence des acides aminés avec le domaine à sept cystéines du C-terminal de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5).

25 **25.** La méthode selon la revendication 24 dans laquelle :

30 (a) le tissu ou organe est tel que défini dans la revendication 15; et/ou
 (b) le morphogène est tel que défini dans la revendication 18 ;
 (c) le morphogène est fourni sous forme d'une solution telle que définie dans la revendication 21 ou 22.

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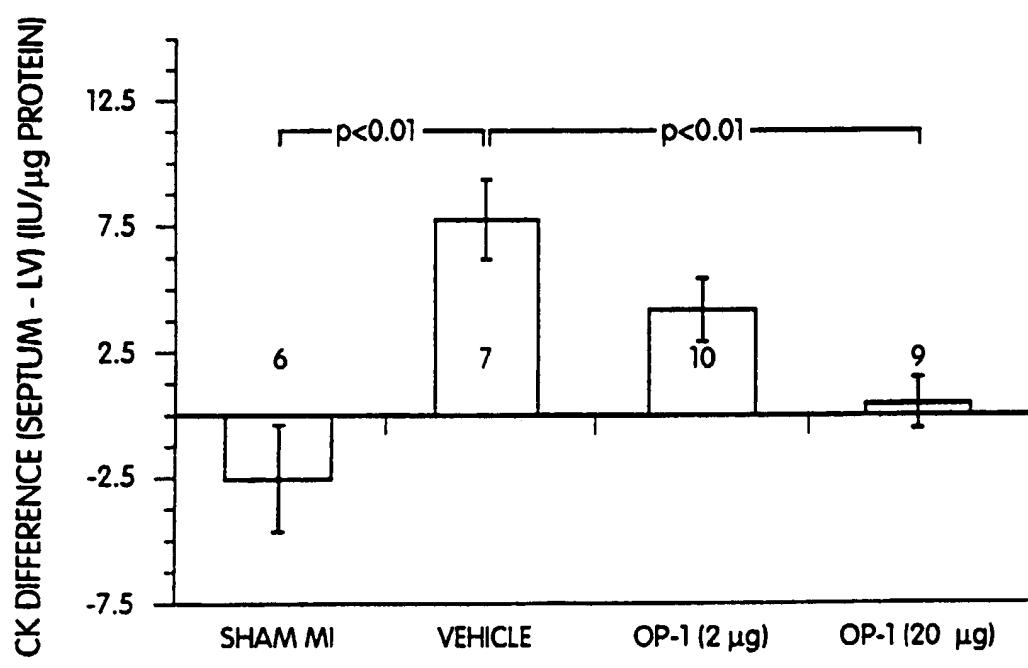


Fig. 1

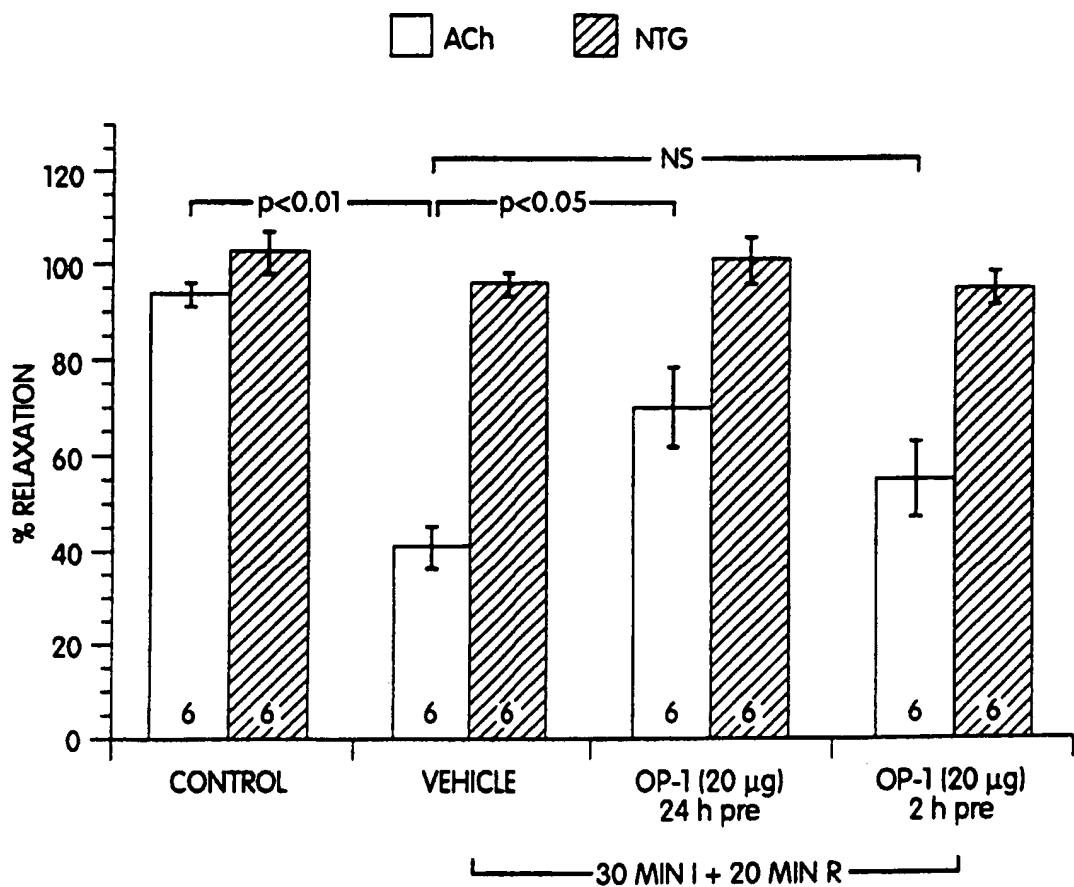


Fig 2

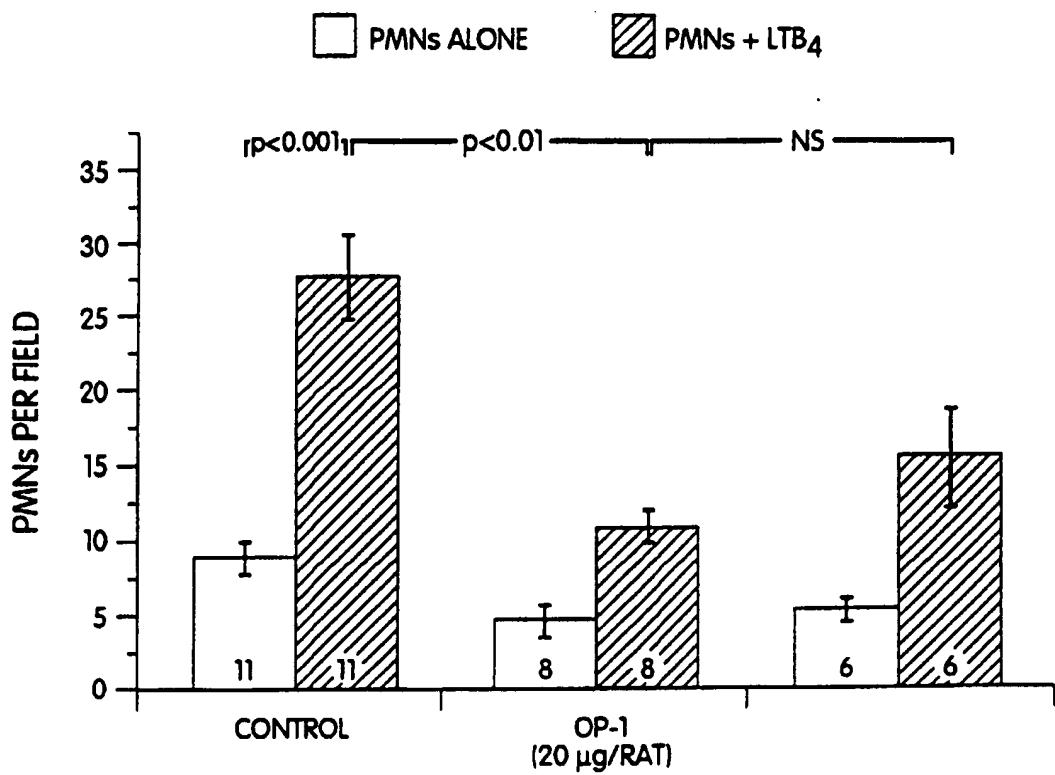


Fig. 3

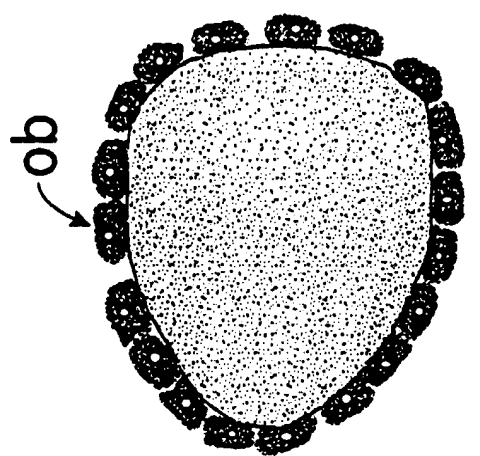


Fig. 4B

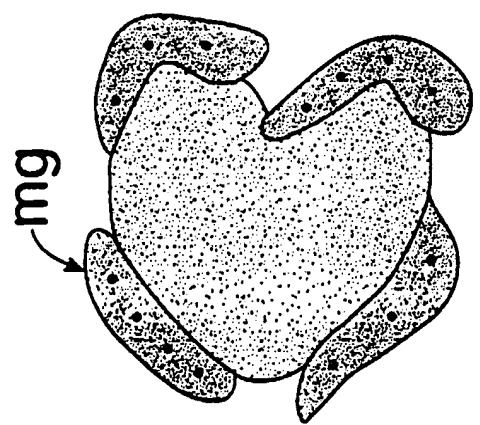


Fig. 4A

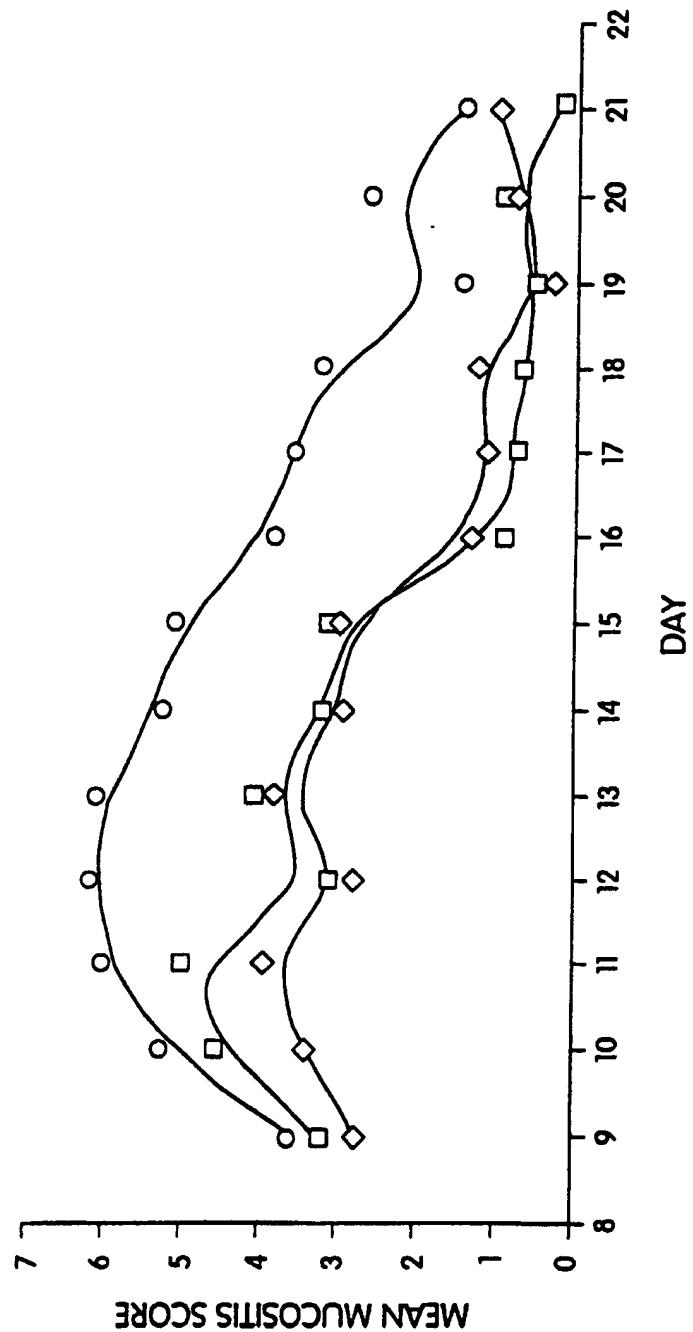


Fig. 5

Fig. 6A

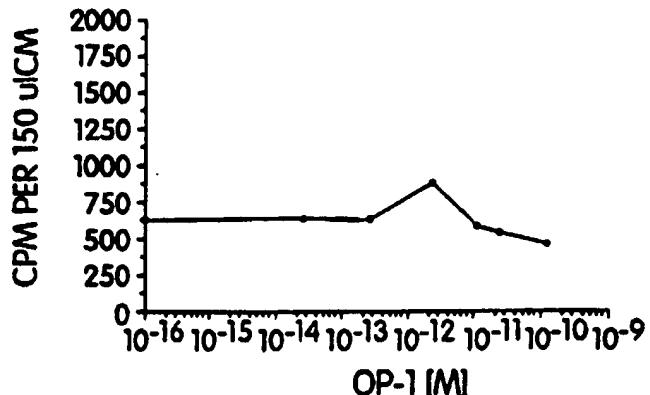


Fig. 6B

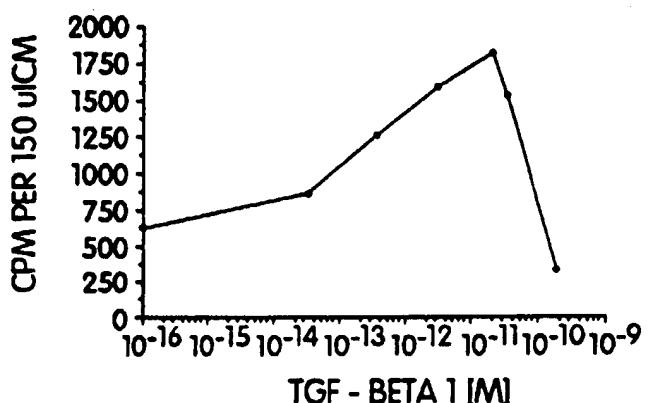


Fig. 6C

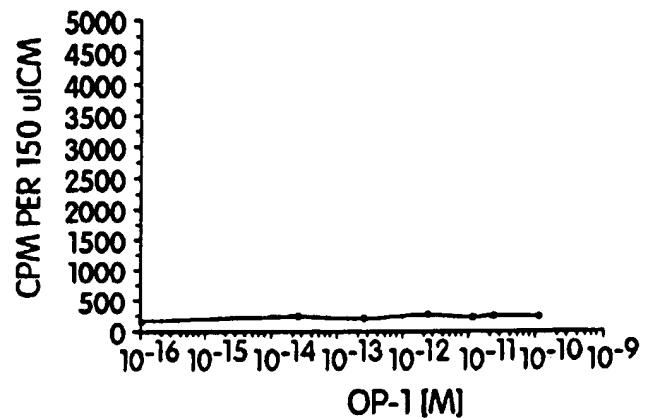
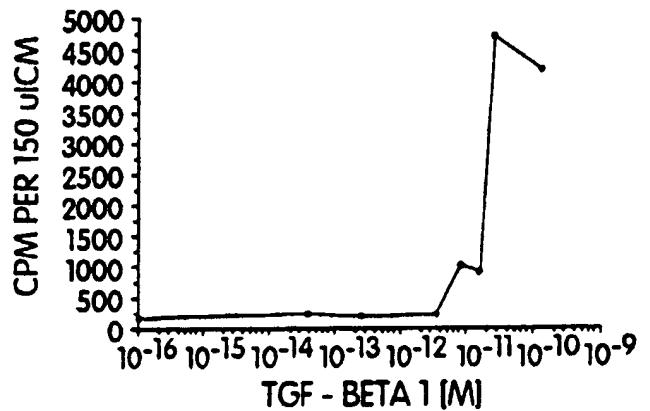


Fig. 6D





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(54) MORPHOGEN-INDUCED MODULATION OF INFLAMMATORY RESPONSE

Morphogen-induzierte Modulation von entzündlichen Antworten

MODULATION, INDUIITE PAR MORPHOGENE, DE REACTION INFLAMMATOIRE

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(73) Proprietor: Curis, Inc.
Cambridge, MA 02138 (US)

(72) Inventors:

- KUBERASAMPATH, Thangavel
Medway, MA 02053 (US)
- PANG, Roy, H., L.
Etna, NH 03750 (US)
- OPPERMANN, Hermann
Medway, MA 02053 (US)
- RUEGER, David, C.
Hopkinton, MA 01748 (US)
- COHEN, Charles, M.
Medway, MA 02053 (US)
- OZKAYNAK, Engin
Milford, MA 01757 (US)
- SMART, John, E.
Weston, MA 02193 (US)

(74) Representative: Price, Vincent Andrew et al
Fry Heath & Spence LLP
The Gables
Massetts Road
Horley Surrey RH6 7DQ (GB)

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Description**Field of the Invention**

5 [0001] The present invention finds generally utility in a method for modulating the inflammatory response induced in a mammal following tissue injury. More particularly, this invention finds utility in a method for alleviating immune-cell mediated tissue destruction associated with the inflammatory response.

Background of the Invention

10 [0002] The body's inflammatory response to tissue injury can cause significant tissue destruction, leading to loss of tissue function. Damage to cells resulting from the effects of inflammatory response e.g., by immune-cell mediated tissue destruction, has been implicated as the cause of reduced tissue function or loss of tissue function in diseases of the joints (e.g., rheumatoid and osteo-arthritis) and of many organs, including the kidney, pancreas, skin, lung and heart. For example, glomular nephritis, diabetes, inflammatory bowel disease, vascular diseases such as atherosclerosis and vasculitis, and skin diseases such as psoriasis and dermatitis are believed to result in large part from unwanted acute inflammatory reaction and fibrosis. A number of these diseases, including arthritis, psoriasis and inflammatory bowel disease are considered to be chronic inflammatory diseases. The damaged tissue also often is replaced by fibrotic tissue, e.g., scar tissue, which further reduces tissue function. Graft and transplanted organ rejection also is believed to be primarily due to the action of the body's immune/inflammatory response system.

15 [0003] The immune-cell mediated tissue destruction often follows an initial tissue injury or insult. The secondary damage, resulting from the inflammatory response, often is the source of significant tissue damage. Among the factors thought to mediate these damaging effects are those associated with modulating the body's inflammatory response following tissue injury, e.g., cytokines such as interleukin-1 (IL-1) and tumor necrosis factor (TNF), and oxygen-derived free radicals such as superoxide anions. These humoral agents are produced by adhering neutrophilic leukocytes or by endothelial cells and have been identified at ischemic sites upon reperfusion. Moreover, TNF concentrations are increased in humans after myocardial infarction.

20 [0004] A variety of lung diseases are characterized by airway inflammation, including chronic bronchitis, emphysema, idiopathic pulmonary fibrosis and asthma. Another type of lung-related inflammation disorders are inflammatory diseases characterized by a generalized, wide-spread acute inflammatory response such as adult respiratory distress syndrome. Another dysfunction associated with the inflammatory response is that mounted in response to injury caused by hyperoxia, e.g., prolonged exposure to lethally high concentrations of O₂ (95-100% O₂). Similarly, reduced blood flow to a tissue (and, therefore reduced or lack of oxygen to tissues), as described below, also can induce a primary tissue injury that stimulates the inflammatory response.

25 [0005] It is well known that damage occurs to cells in mammals which have been deprived of oxygen. In fact, the interruption of blood flow, whether partial (hypoxia) or complete (ischemia) and the ensuing inflammatory responses may be the most important cause of coagulative necrosis or cell death in human disease. The complications of atherosclerosis, for example, are generally the result of ischemic cell injury in the brain, heart, small intestines, kidneys, and lower extremities. Highly differentiated cells, such as the proximal tubular cells of the kidney, cardiac myocytes, and 30 the neurons of the central nervous system, all depend on aerobic respiration to produce ATP, the energy necessary to carry out their specialized functions. When ischemia limits the oxygen supply and ATP is depleted, the affected cells may become irreversibly injured. The ensuing inflammatory responses to this initial injury provide additional insult to the affected tissue. Examples of such hypoxia or ischemia are the partial or total loss of blood supply to the body as a whole, an organ within the body, or a region within an organ, such as occurs in cardiac arrest, pulmonary embolus, renal artery occlusion, coronary occlusion or occlusive stroke.

35 [0006] The tissue damage associated with ischemia-reperfusion injury is believed to comprise both the initial cell damage induced by the deprivation of oxygen to the cell and its subsequent recirculation, as well as the damage caused by the body's response to this initial damage. It is thought that reperfusion injury may result in dysfunction to the endothelium of the vasculature as well as injury to the surrounding tissue. In idiopathic pulmonary fibrosis, for example, 40 scar tissue accumulates on the lung tissue lining, inhibiting the tissue's elasticity. The tissue damage associated with hyperoxia injury is believed to follow a similar mechanism, where the initial damage is mediated primarily through the presence of toxic oxygen metabolites followed by an inflammatory response to this initial injury.

45 [0007] Similarly, tissues and organs for transplantation also are subject to the tissue destructive effects associated with the recipient host body's inflammatory response following transplantation. It is currently believed that the initial destructive response is due in large part to reperfusion injury to the transplanted organ after it has been transplanted to the organ recipient.

50 [0008] Accordingly, the success of organ or tissue transplantation depends greatly on the preservation of the tissue activity (e.g., tissue or organ viability) at the harvest of the organ, during storage of the harvested organ, and at trans-

plantation. To date, preservation of organs such as lungs, pancreas, heart and liver remains a significant stumbling block to the successful transplantation of these organs. U.S. Patent No. 4,952,409 describes a superoxide dismutase-containing liposome to inhibit reperfusion injury. U.S. Patent No. 5,002,965 describes the use of ginkolides, known platelet activating factor antagonists, to inhibit reperfusion injury. Both of these factors are described working primarily by inhibiting the release of and/or inhibiting the damaging effects of free oxygen radicals. A number of patents also have issued on the use of immunosuppressants for inhibiting graft rejection. A representative listing includes U.S. Patent Nos. 5,104,858, 5,008,246 and 5,068,323. A significant problem with many immunosuppressants is their low therapeutic index, requiring the administration of high doses that can have significant toxic side effects.

[0009] Rheumatoid and osteoarthritis are prevalent diseases characterized by chronic inflammation of the synovial membrane lining the afflicted joint. A major consequence of chronic inflammatory joint disease (e.g., rheumatoid arthritis) and degenerative arthritis (e.g., osteoarthritis) is loss of function of those affected joints. This loss of function is due primarily to destruction of the major structural components of the joint, cartilage and bone, and subsequent loss of the proper joint anatomy. As a consequence of chronic disease, joint destruction ensues and can lead to irreversible and permanent damage to the joint and loss of function. Current treatment methods for severe cases of rheumatoid arthritis typically include the removal of the synovial membrane, e.g., synovectomy. Surgical synovectomy has many limitations, including the risk of the surgical procedure itself, and the fact that a surgeon often cannot remove all of the diseased membrane. The diseased tissue remaining typically regenerates, causing the same symptoms which the surgery was meant to alleviate.

[0010] Psoriasis is a chronic, recurrent, scaling skin disease of unknown etiology characterized by chronic inflammation of the skin. Erythematous eruptions, often in papules or plaques, and usually having a white silvery scale, can affect any part of the skin, but most commonly affect the scalp, elbows, knees and lower back. The disease usually occurs in adults, but children may also be affected. Patients with psoriasis have a much greater incidence of arthritis (psoriatic arthritis), and generalized exfoliation and even death can threaten afflicted individuals.

[0011] Current therapeutic regimens include topical or intralesional application of corticosteroids, topical administration of keratolytics, and use of tar and UV light on affected areas. No single therapy is ideal, and it is rare for a patient not to be treated with several alternatives during the relapsing and remitting course of the disease. Whereas systematic treatment can induce prompt resolution of psoriatic lesions, suppression often requires ever-increasing doses, sometimes with toxic side effect, and tapering of therapy may result in rebound phenomena with extensions of lesions, possibly to exfoliation.

[0012] Inflammatory bowel disease (IBD) describes a class of clinical disorders of the gastrointestinal mucosa characterized by chronic inflammation and severe ulceration of the mucosa. The two major diseases in this classification are ulcerative colitis and regional enteritis (Crohn's Disease). Like oral mucositis, the diseases classified as IBD are associated with severe mucosal ulceration (frequently penetrating the wall of the bowel and forming strictures and fistulas), severe mucosal and submucosal inflammation and edema, and fibrosis (e.g., scar tissue formation which interferes with the acid protective function of the gastrointestinal lining.) Other forms of IBD include regional ileitis and proctitis. Clinically, patients with fulminant IBD can be severely ill with massive diarrhea, blood loss, dehydration, weight loss and fever. The prognosis of the disease is not good and frequently requires resection of the diseased tissue.

[0013] The present invention finds application in a method for protecting mammalian tissue, particularly human tissue, from the damage associated with the inflammatory response following a tissue injury. The inflammatory reaction may be in response to an initial tissue injury or insult. The original injury may be chemically, mechanically, biologically or immunologically related. Another application is in methods and compositions for protecting tissue from the tissue destructive effects associated with chronic inflammatory diseases, including arthritis (e.g., rheumatoid or osteoarthritis), psoriatic arthritis, psoriasis and dermatitis, inflammatory bowel disease and other autoimmune diseases. Yet another application is in methods and compositions for enhancing the viability of mammalian tissues and organs to be transplanted, including protecting the transplanted organs from immune cell-mediated tissue destruction, such as the tissue damage associated with ischemia-reperfusion injury. This tissue damage may occur during donor tissue or organ harvesting and transport, as well as following initiation of blood flow after transplantation of the organ or tissue in the recipient host.

[0014] The invention also finds application in a method for alleviating tissue damage associated with ischemic-reperfusion injury in a mammal following a deprivation of oxygen to a tissue in the mammal. Other applications include providing a method for alleviating tissue damage associated with ischemic-reperfusion injury in a human which has suffered from hypoxia or ischemia following cardiac arrest, pulmonary embolus, renal artery occlusion, coronary occlusion or occlusive stroke. A further application is to provide a method for alleviating tissue damage associated with hyperoxia-induced tissue injury, e.g., lethally high oxygen concentrations.

[0015] Still another application of the invention is to provide a method for modulating inflammatory responses in general, particularly those induced in a human following tissue injury.

[0016] These and other objects and features of the invention will be apparent from the description, drawings and claims which follow.

[0017] Each of Kurvilla et al. (1991), 88 Proc. Natl. Acad. Sci. USA 2918-2921, Lefer et al. (1990), 249 Science 61-64; Shepard et. al., EP 0,269,408; Nathan et al., W090/00900; and, Bentz et al., U.S. Pat. 4,971,952 describe studies testing whether TGF β can mitigate specific types of inflammatory or ischemia reperfusion damage to mammalian cells or tissues. TGF- β is not a member of the class of proteins defined herein as morphogens.

5 [0018] Each of Oppermann et. al., W091/05802; Kuberampath et al., WO89/09787; Oppermann et al., WO89/09788; and Oppermann et al. W092/07073 teach that OP-1 and related proteins may be used in stimulating tissue-specific regeneration of mammalian cartilage and bone tissue. In particular, these references teach that OP-1, when adsorbed on a suitable supporting matrix, induces the developmental cascade of cellular and molecular events that culminates in endochondral bone morphogenesis. The biologically active OP-1 preparations are taught to be, at best, sparingly soluble in physiologically compatible solutions. OP-1-charged matrix devices thus are disclosed as useful for inducing local morphogenesis of bone and/or cartilage.

10 [0019] Cohen et al., W092/15323 teaches that OP-1 induces tissue specific morphogenesis in diverse mammalian body tissues, and that morphogen can be used in the replacement or repair of damaged tissues.

15 **Summary of the Invention**

[0020] The present invention is defined in the claims. It finds utility in a method for alleviating the tissue destructive effects associated with activation of the inflammatory response following tissue injury. The method comprises the step of providing to the affected tissue a therapeutically effective concentration of a morphogenic protein ("morphogen", as defined herein) upon tissue injury or in anticipation of tissue injury, sufficient to substantially inhibit or reduce the tissue destructive effects of the inflammatory response.

20 [0021] Also described herein are compositions and therapeutic treatment methods that comprise the step of administering to a mammal a therapeutically effective amount of a morphogenic protein ("morphogen"), as defined herein, upon injury to a tissue, or in anticipation of such injury, for a time and at a concentration sufficient to inhibit the tissue 25 destructive effects associated with the body's inflammatory response, including repairing damaged tissue, and/or inhibiting additional damage thereto.

[0022] As embodied herein, the term "ischemic-reperfusion injury" refers to the initial damage associated with oxygen deprivation of a cell and the subsequent damage associated with the inflammatory response when the cell is resupplied with oxygen. As embodied herein, the term "hyperoxia-induced injury" refers to the tissue damage associated with 30 prolonged exposure to lethally high doses of oxygen, e.g., greater than 95% O₂, including the tissue damage associated with the inflammatory response to the toxicologically high oxygen dose. Accordingly, as used herein, "toxic oxygen concentrations" refers to the tissue damage associated with the injury induced by both lethally low oxygen concentrations of oxygen (including a complete lack of oxygen), and by lethally high oxygen concentrations. The expression "alleviating" means the protection from, reduction of and/or elimination of undesired tissue destruction, particularly immune cell-mediated tissue destruction. The tissue destruction may be in response to an initial tissue injury, which may be mechanical, chemical or immunological in origin. The expression "enhance the viability of" living tissues or organs, as 35 used herein, means protection from, reduction of and/or elimination of reduced or lost tissue or organ function as a result of tissue death, particularly immune cell-mediated tissue death. "Transplanted" living tissue encompasses both tissue transplants (e.g., as in the case of bone marrow transplants) and tissue grafts. Finally, a "free oxygen radical inhibiting agent" means a molecule capable of inhibiting the release of and/or inhibiting tissue damaging effects of free 40 oxygen radicals.

[0023] Described herein are methods and compositions for alleviating the ischemic-reperfusion injury in mammalian tissue resulting from a deprivation of, and subsequent reperfusion of, oxygen to the tissue. Also described is a method for alleviating the tissue-destructive effects associated with hyperoxia. Methods and compositions for maintaining the 45 viability of tissues and organs, particularly living tissues and organs to be transplanted, including protecting them from ischemia-reperfusion injury, together with methods for protecting tissues and organs from the tissue destructive effects of chronic inflammatory diseases, such as arthritis, psoriasis, dermatitis, including contact dermatitis, IBD and other chronic inflammatory diseases of the gastrointestinal tract, as well as the tissue destructive effects associated with other, known autoimmune diseases, such as diabetes, multiple sclerosis, amyotrophic lateral sclerosis (ALS), and 50 other autoimmune neurodegenerative diseases are also described herein.

[0024] The morphogen may be provided to the damaged tissue following an initial injury to the tissue. The morphogen may be provided directly to the tissue, as by injection to the damaged tissue site or by topical administration, or may be provided indirectly, e.g., systemically by oral or parenteral means.

[0025] The morphogen may also be provided to tissue at risk of damage due to immune cell-mediated tissue destruction. Examples of such tissues include tissue grafts and tissue or organ transplants, as well as any tissue or organ about to undergo a surgical procedure or other clinical procedure likely to either inhibit blood flow to the tissue or otherwise induce an inflammatory response. Here the morphogen preferably is provided to the patient prior to induction of the injury, e.g., as a prophylactic, to provide a cyto-protective effect to the tissue at risk.

[0026] Where the tissue at risk comprises a tissue or organ to be transplanted, the tissue or organ to be transplanted preferably is exposed to a morphogen prior to transplantation. Most preferably, the tissue or organ is exposed to the morphogen prior to its removal from the donor, by providing the donor with a composition comprising a morphogen. Alternatively or, in addition, once removed from the donor, the organ or tissue is placed in a preservation solution containing a morphogen. In addition, the recipient also preferably is provided with a morphogen just prior to, or con-committant with, transplantation. In all cases, the morphogen may be administered directly to the tissue at risk, as by injection or topical administration to the tissue, or it may be provided systemically, either by oral or parenteral administration.

[0027] The morphogens described herein are envisioned to be useful in enhancing viability of any organ or living tissue to be transplanted. The morphogens may be used to particular advantage in lung, heart, liver, kidney or pancreas transplants, as well as in transplantation and/or grafting of bone marrow, skin, gastrointestinal mucosa, and other living tissues.

[0028] Where the patient suffers from a chronic inflammatory disease, such as diabetes, arthritis, psoriasis, IBD, and the like, the morphogen preferably is administered at regular intervals as a prophylactic, to prevent and/or inhibit the tissue damage normally associated with the disease during flare periods. As above, the morphogen may be provided directly to the tissue at risk, for example by injection or by topical administration, or indirectly, as by systemic e.g., oral or parenteral administration.

[0029] Among the morphogens useful in this invention are proteins originally identified as osteogenic proteins, such as the OP-1, OP-2 and CBMP2 proteins, as well as amino acid sequence-related proteins such as DPP (from *Drosophila*), Vgl (from *Xenopus*), Vgr-1 (from mouse, see U.S. 5,011,691 to Oppermann et al.), GDF-1 (from mouse, see Lee (1991) *PNAS* 88:4250-4254), all of which are presented in Table II and Seq. ID Nos. 5-14), and the recently identified 60A protein (from *Drosophila*, Seq. ID No. 24, see Wharton et al. (1991) *PNAS* 88:9214-9218.) The members of this family, which include members of the TGF- β super-family of proteins, share substantial amino acid sequence homology in their C-terminal regions. The proteins are translated as a precursor, having an N-terminal signal peptide sequence, typically less than about 30 residues, followed by a "pro" domain that is cleaved to yield the mature sequence. The signal peptide is cleaved rapidly upon translation, at a cleavage site that can be predicted in a given sequence using the method of Von Heijne ((1986) *Nucleic Acids Research* 14:4683-4691.) Table I, below, describes the various morphogens identified to date, including their nomenclature as used herein, their Seq. ID references, and publication sources for the amino acid sequences for the full length proteins not included in the Seq. Listing.

30

TABLE I

	"OP-1"	Refers generically to the group of morphogenically active proteins expressed from part or all of a DNA sequence encoding OP-1 protein, including allelic and species variants thereof, e.g., human OP-1 ("hOP-1", Seq. ID No. 5, mature protein amino acid sequence), or mouse OP-1 ("mOP-1", Seq. ID No. 6, mature protein amino acid sequence.) The conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 5 and 6. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. Id Nos. 16 and 17 (hOP1) and Seq. ID Nos. 18 and 19 (mOP1.) The mature proteins are defined by residues 293-431 (hOP1) and 292-430 (mOP1). The "pro" regions of the proteins, cleaved to yield the mature, morphogenically active proteins are defined essentially by residues 30-292 (hOP1) and residues 30-291 (mOP1).
	"OP-2"	Refers generically to the group of active proteins expressed from part or all of a DNA sequence encoding OP-2 protein, including allelic and species variants thereof, e.g., human OP-2 ("hOP-2", Seq. ID No. 7, mature protein amino acid sequence) or mouse OP-2 ("mOP-2", Seq. ID No. 8, mature protein amino acid sequence). The conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 7 and 8. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 20 and 21 (hOP2) and Seq. ID Nos. 22 and 23 (mOP2.) The mature proteins are defined essentially by residues 264-402 (hOP2) and 261-399 (mOP2). The "pro" regions of the proteins, cleaved to yield the mature, morphogenically active proteins likely are defined essentially by residues 18-263 (hOP2) and residues 18-260 (mOP2). (Another cleavage site also occurs 21 residues upstream for both OP-2 proteins.)

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TABLE I (continued)

	"CBMP2"	refers generically to the morphogenically active proteins expressed from a DNA sequence encoding the CBMP2 proteins, including allelic and species variants thereof, e.g., human CBMP2A ("CBMP2A (fx)", Seq ID No. 9) or human CBMP2B DNA ("CBMP2B(fx)", Seq. ID No. 10). The amino acid sequence for the full length proteins, referred to in the literature as BMP2A and BMP2B, or BMP2 and BMP4, appear in Wozney, et al. (1988) <i>Science</i> 242:1528-1534. The pro domain for BMP2 (BMP2A) likely includes residues 25-248 or 25-282; the mature protein, residues 249-396 or 283-396. The pro domain for BMP4 (BMP2B) likely includes residues 25-256 or 25-292; the mature protein, residues 257-408 or 293-408.
5	"DPP(fx)"	refers to protein sequences encoded by the Drosophila DPP gene and defining the conserved seven cysteine skeleton (Seq. ID No. 11). The amino acid sequence for the full length protein appears in Padgett, et al (1987) <i>Nature</i> 325: 81-84. The pro domain likely extends from the signal peptide cleavage site to residue 456; the mature protein likely is defined by residues 457-588.
10	"Vgl(fx)"	refers to protein sequences encoded by the Xenopus Vgl gene and defining the conserved seven cysteine skeleton (Seq. ID No. 12). The amino acid sequence for the full length protein appears in Weeks (1987) <i>Cell</i> 51: 861-867. The prodomain likely extends from the signal peptide cleavage site to residue 246; the mature protein likely is defined by residues 247-360.
15	"Vgr-1(fx)"	refers to protein sequences encoded by the murine Vgr-1 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 13). The amino acid sequence for the full length protein appears in Lyons, et al, (1989) <i>PNAS</i> 86: 4554-4558. The prodomain likely extends from the signal peptide cleavage site to residue 299; the mature protein likely is defined by residues 300-438.
20	"GDF-1(fx)"	refers to protein sequences encoded by the human GDF-1 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 14). The cDNA and encoded amino sequence for the full length protein is provided in Seq. ID. No. 32. The prodomain likely extends from the signal peptide clavage site to residue 214; the mature protein likely is defined by residues 215-372.
25	"60A"	refers generically to the morphogenically active proteins expressed from part or all of a DNA sequence (from the Drosophila 60A gene) encoding the 60A proteins (see Seq. ID No. 24 wherein the cDNA and encoded amino acid sequence for the full length protein is provided). "60A(fx)" refers to the protein sequences defining the conserved seven cysteine skeleton (residues 354 to 455 of Seq. ID No. 24.) The prodomain likely extends from the signal peptide cleavage site to residue 324; the mature protein likely is defined by residues 325-455.
30	"BMP3(fx)"	refers to protein sequences encoded by the human BMP3 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 26). The amino acid sequence for the full length protein appears in Wozney et al. (1988) <i>Science</i> 242: 1528-1534. The pro domain likely extends from the signal peptide cleavage site to residue 290; the mature protein likely is defined by residues 291-472.
35	"BMP5(fx)"	refers to protein sequences encoded by the human BMP5 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 27). The amino acid sequence for the full length protein appears in Celeste, et al. (1991) <i>PNAS</i> 87: 9843-9847. The pro domain likely extends from the signal peptide cleavage site to residue 316; the mature protein likely is defined by residues 317-454.
40	"BMP6(fx)"	refers to protein sequences encoded by the human BMP6 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 28). The amino acid sequence for the full length protein appears in Celeste, et al. (1990) <i>PNAS</i> 87: 9843-5847. The pro domain likely includes extends from the signal peptide cleavage site to residue 374; the mature sequence likely includes residues 375-513.
45		

[0030] The OP-2 proteins have an additional cysteine residue in this region (e.g., see residue 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The GDF-1 protein has a four amino acid insert within the conserved skeleton (residues 44-47 of Seq. ID No. 14) but this insert likely does not interfere with the relationship of the cysteines in the folded structure. In addition, the CBMP2 proteins are missing one amino acid residue within the cysteine skeleton.

[0031] The morphogens are inactive when reduced, but are active as oxidized homodimers and when oxidized in combination with other morphogens (e.g., as heterodimers). Thus, as defined herein, a morphogen is a dimeric protein comprising a pair of polypeptide chains, wherein each polypeptide chain comprises at least the C-terminal six cysteine skeleton defined by residues 43-139 of Seq. ID No. 5 including functionally equivalent arrangements of these cysteines (e.g., amino acid insertions or deletions which alter the linear arrangement of the cysteines in the sequence but not

their relationship in the folded structure), such that, when the polypeptide chains are folded, the dimeric protein species comprising the pair of polypeptide chains has the appropriate three-dimensional structure, including the appropriate intra-or inter-chain disulfide bonds such that the protein is capable of acting as a morphogen as defined herein. Specifically, the morphogens generally are capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. In addition, it is also anticipated that these morphogens are capable of inducing redifferentiation of committed cells under appropriate environmental conditions.

[0032] The morphogens described herein may comprise one of two species of generic amino acid sequences: Generic Sequence 1 (Seq. ID No. 1) or Generic Sequence 2 (Seq. ID No. 2); where each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof. Generic Sequence 1 comprises the conserved six cysteine skeleton and Generic Sequence 2 comprises the conserved six cysteine skeleton plus the additional cysteine identified in OP-2 (see residue 36 Seq. ID No. 2). These sequences may further comprise the following additional sequence at their N-terminus:

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Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)
1 5

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[0033] Amino acid sequences within the foregoing generic sequences include: Generic Sequence 3 (Seq. ID No. 3), Generic Sequence 4 (Seq. ID No. 4), Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31), listed below. These Generic Sequences accommodate the homologies shared among the various preferred members of this morphogen family identified in Table II, as well as the amino acid sequence variation among them. Specifically, Generic Sequences 3 and 4 are composite amino acid sequences of the following proteins presented in Table II and identified in Seq. ID Nos. 5-14: human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from *Drosophila*, Seq. ID No. 11), Vgl, (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14.) The generic sequences include both the amino acid identity shared by the sequences in Table II, as well as alternative residues for the variable positions within the sequence. Note that these generic sequences allow for an additional cysteine at position 41 or 46 in Generic Sequences 3 or 4, respectively, providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins.

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Generic Sequence 3

	Leu	Tyr	Val	Xaa	Phe
5					
	1			5	
	Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa				
10			10		
	Xaa Ala Pro Xaa Gly Xaa Xaa Ala				
	15		20		
15	Xaa Tyr Cys Xaa Gly Xaa Cys Xaa				
	25		30		
20	Xaa Pro Xaa Xaa Xaa Xaa Xaa				
	35				
	Xaa Xaa Xaa Asn His Ala Xaa Xaa				
25	40		45		
	Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa				
	50				
30	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys				
	55		60		
35	Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa				
	65				
40	Xaa Xaa Xaa Leu Xaa Xaa Xaa				
	70		75		
45	Xaa Xaa Xaa Xaa Val Xaa Leu Xaa				
	80				
50	Xaa Xaa Xaa Xaa Met Xaa Val Xaa				
	85		90		
	Xaa Cys Gly Cys Xaa				
55	95				

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows:

"Res." means "residue" and Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser or Lys); Xaa at res.7 = (Asp or Glu); Xaa at res.8 = (Leu or Val); Xaa at res.11 = (Gln, Leu, Asp, His or Asn); Xaa at res.12 = (Asp, Arg or Asn); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Leu or Gln); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at res.26 = (Glu, His, Tyr, Asp or Gln); Xaa at res.28 = (Glu, Lys, Asp or Gln); Xaa at res.30 = (Ala, Ser, Pro or Gln); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu or Val); Xaa at res.34 = (Asn, Asp, Ala or Thr); Xaa at res.35 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn or Ser); Xaa at res.39 = (Ala, Ser or Gly); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile or Val); Xaa at res.45 = (Val or Leu); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His or Asn); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala or Val); Xaa at res.53 = (Asn, Lys, Ala or Glu); Xaa at res.54 = (Pro or Ser); Xaa at res.55 = (Glu, Asp, Asn, or Gly); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys or Leu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr or Ala); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser or Asp); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr or Val); Xaa at res.71 = (Ser or Ala); Xaa at res.72 = (Val or Met); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr or Leu); Xaa at res.76 = (Asp or Asn); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn or Tyr); Xaa at res.79 = (Ser, Asn, Asp or Glu); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile or Val); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln or His); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln or Glu); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr or Ala); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly or Glu); and Xaa at res.97 = (His or Arg);

Generic Sequence 4

25 Cys Xaa Xaa Xaa Xaa Leu Tyr Val Xaa Phe
 1 5 10
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 30 15
 Xaa Ala Pro Xaa Gly Xaa Xaa Ala
 20 25
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 30 35

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	Xaa Pro Xaa Xaa Xaa Xaa Xaa		
5		40	
	Xaa Xaa Xaa Asn His Ala Xaa Xaa		
		45	50
10	Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa		
		55	
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys		
		60	65
15	Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa		
		70	
	Xaa Xaa Xaa Leu Xaa Xaa Xaa		
		75	80
20	Xaa Xaa Xaa Xaa Val Xaa Leu Xaa		
		85	
	Xaa Xaa Xaa Xaa Met Xaa Val Xaa		
		90	95
25	Xaa Cys Gly Cys Xaa		
		100	

30 wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys or Arg); Xaa at res.3 = (Lys or Arg); Xaa at res.4 = (His or Arg); Xaa at res.5 = (Glu, Ser, His, Gly, Arg or Pro); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser or Lys); Xaa at res.12 = (Asp or Glu); Xaa at res.13 = (Leu or Val); Xaa at res.16 = (Gln, Leu, Asp, His or Asn); Xaa at res.17 = (Asp, Arg, or Asn); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Leu, or Gln); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp or Gln); Xaa at res.33 = (Glu, Lys, Asp or Gln); Xaa at res.35 = (Ala, Ser or Pro); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu or Val); Xaa at res.39 = (Asn, Asp, Ala or Thr); Xaa at res.40 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.44 = (Ala, Ser or Gly); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile or Val); Xaa at res.50 = (Val or Leu); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His or Asn); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala or Val); Xaa at res.58 = (Asn, Lys, Ala or Glu); Xaa at res.59 = (Pro or Ser); Xaa at res.60 = (Glu, Asp, or Gly); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys or Leu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr or Ala); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser or Asp); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr or Val); Xaa at res.76 = (Ser or Ala); Xaa at res.77 = (Val or Met); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr or Leu); Xaa at res.81 = (Asp or Asn); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn or Tyr); Xaa at res.84 = (Ser, Asn, Asp or Glu); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile or Val); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln or His); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln or Glu); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr or Ala); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly or Glu); and Xaa at res.102 = (His or Arg).

[0034] Similarly, Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31) accommodate the homologies shared among all the morphogen protein family members identified in Table II. Specifically, Generic Sequences 5 and 6 are composite amino acid sequences of human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14), human BMP3 (Seq. ID No. 26), human BMP5 (Seq. ID No. 27), human BMP6 (Seq. ID No. 28) and 60(A) (from Drosophila, Seq. ID Nos. 24-25). The generic

5 sequences include both the amino acid identity shared by these sequences in the C-terminal domain, defined by the six and seven cysteine skeletons (Generic Sequences 5 and 6, respectively), as well as alternative residues for the variable positions within the sequence. As for Generic Sequences 3 and 4, Generic Sequences 5 and 6 allow for an additional cysteine at position 41 (Generic Sequence 5) or position 46 (Generic Sequence 6), providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and containing certain critical amino acids which influence the tertiary structure of the proteins.

10 Generic Sequence 5

Leu Xaa Xaa Xaa Phe

15 1 5

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

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	Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala	
5	15	20
	Xaa Tyr Cys Xaa Gly Xaa Cys Xaa	
	25	30
10	Xaa Pro Xaa Xaa Xaa Xaa Xaa	
		35
15	Xaa Xaa Xaa Asn His Ala Xaa Xaa	
	40	45
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	
20		50
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys	
25	55	60
	Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa	
		65
30	Xaa Xaa Xaa Leu Xaa Xaa Xaa	
	70	75
	Xaa Xaa Xaa Xaa Val Xaa Leu Xaa	
35		80
	Xaa Xaa Xaa Xaa Met Xaa Val Xaa	
40	85	90
	Xaa Cys Xaa Cys Xaa	
45		95

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows: "Res." means "residue" and Xaa at res.2 = (Tyr or Lys); Xaa at res.3 = Val or Ile); Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.7 = (Asp, Glu or Lys); Xaa at res.8 = (Leu, Val or Ile); Xaa at res.11 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.12 = (Asp, Arg, Asn or Glu); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.16 = (Ala or Ser); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.19 = (Gly or Ser); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Gln, Leu or Gly); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at res.26 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.28 = (Glu, Lys, Asp, Gln or Ala); Xaa at res.30 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu, Val or Met); Xaa at res.34 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.35 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn, Ser or Lys); Xaa at res.39 = (Ala, Ser, Gly or Pro); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile, Val or Thr); Xaa at res.45 = (Val, Leu or Ile); Xaa at res.46 = (Gin or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.48 = (Leu or Ile); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His, Asn or Arg); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.53 =

(Asn, Lys, Ala, Glu, Gly or Phe); Xaa at res.54 = (Pro, Ser or Val); Xaa at res.55 = (Glu, Asp, Asn, Gly, Val or Lys); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys, Leu or Glu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr, Ala or Glu); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser, Asp or Gly); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr, Val or Leu); Xaa at res.71 = (Ser, Ala or Pro); Xaa at res.72 = (Val, Met or Ile); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr, Leu or His); Xaa at res.76 = (Asp, Asn or Leu); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.79 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile, Val or Asn); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln, His or Val); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln, Glu or Pro); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr, Ala or Ile); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly, Glu or Ser); Xaa at res.95 = (Gly or Ala) and Xaa at res.97 = (His or Arg).

Generic Sequence 6

15

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
 1 5 10

20

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 15

25

Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 20 25
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 30 35

30

Xaa Pro Xaa Xaa Xaa Xaa Xaa
 40

35

Xaa Xaa Xaa Asn His Ala Xaa Xaa
 45 50

40

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60 65
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 70

45

Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75 80

50

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 85

55

Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90 95
 Xaa Cys Xaa Cys Xaa
 100

wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys, Arg, Ala or Gln); Xaa at res.3 = (Lys, Arg or Met); Xaa at res.4 = (His, Arg or Gln); Xaa at res.5 = (Glu, Ser, His, Gly, Arg, Pro, Thr, or Tyr); Xaa at res.7 = (Tyr or Lys); Xaa at res.8 = (Val or Ile); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.12 = (Asp, Glu, or Lys); Xaa at res.13 = (Leu, Val or Ile); Xaa at res.16 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.17 = (Asp, Arg, Asn or Glu); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.21 = (Ala or Ser); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.24 = (Gly or Ser); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Gln, Leu, or Gly); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.33 = Glu, Lys, Asp, Gln or Ala); Xaa at res.35 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu, Val or Met); Xaa at res.39 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.40 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.43 = (Asn, Ser or Lys); Xaa at res.44 = (Ala, Ser, Gly or Pro); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile, Val or Thr); Xaa at res.50 = (Val, Leu or Ile); Xaa at res.51 = (Gin or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.53 = (Leu or Ile); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His, Asn or Arg); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.58 = (Asn, Lys, Ala, Glu, Gly or Phe); Xaa at res.59 = (Pro, Ser or Val); Xaa at res.60 = (Glu, Asp, Gly, Val or Lys); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys, Leu or Glu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr, Ala or Glu); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser, Asp or Gly); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr, Val or Leu); Xaa at res.76 = (Ser, Ala or Pro); Xaa at res.77 = (Val, Met or Ile); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr, Leu or His); Xaa at res.81 = (Asp, Asn or Leu); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.84 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile, Val or Asn); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln, His or Val); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gin, Glu or Pro); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr, Ala or Ile); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly, Glu or Ser); Xaa at res.100 = (Gly or Ala); and Xaa at res.102 = (His or Arg).

[0035] Particularly useful sequences for use as morphogens in this invention include the C-terminal domains, e.g., the C-terminal 96-102 amino acid residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B, GDF-1 (see Table II, below, and Seq. ID Nos. 5-14), as well as proteins comprising the C-terminal domains of 60A, BMP3, BMP5 and BMP6 (see Seq. ID Nos. 24-28), all of which include at least the conserved six or seven cysteine skeleton. In addition, biosynthetic constructs designed from the generic sequences, such as COP-1, 3-5, 7, 16, disclosed in U.S. Pat. No. 5,011,691, also are useful. In another preferred aspect of the invention, useful morphogens include active proteins comprising species of polypeptide chains having the generic amino acid sequence herein referred to as "OPX", which accommodates the homologies between the various identified species of OP1 and OP2 (Seq. ID No. 29).

[0036] The morphogens described herein include proteins comprising any of the polypeptide chains described above, whether isolated from naturally-occurring sources, or produced by recombinant DNA or other synthetic techniques, and includes allelic and species variants of these proteins, naturally-occurring or biosynthetic mutants thereof, as well as various truncated and fusion constructs. Deletion or addition mutants also are envisioned to be active, including those which may alter the conserved C-terminal cysteine skeleton, provided that the alteration does not functionally disrupt the relationship of these cysteines in the folded structure. Accordingly, such active forms are considered the equivalent of the specifically described constructs disclosed herein.

[0037] The proteins may include forms having varying glycosylation patterns, varying N-termini, a family of related proteins having regions of amino acid sequence homology, and active truncated or mutated forms of native or biosynthetic proteins, produced by expression of recombinant DNA in host cells.

[0038] The morphogenic proteins can be expressed from intact or truncated cDNA or from synthetic DNAs in prokaryotic or eucaryotic host cells, and purified, cleaved, refolded, and dimerized to form morphogenically active compositions. Currently preferred host cells include *E. coli* or mammalian cells, such as CHO, COS or BSC cells.

[0039] Thus, in view of this disclosure, skilled genetic engineers can isolate genes from cDNA or genomic libraries of various different species which encode appropriate amino acid sequences, or construct DNAs from oligonucleotides, and then can express them in various types of host cells, including both prokaryotes and eucaryotes, to produce large quantities of active proteins capable of protecting tissues and organs from immune cell-mediated tissue destruction, including substantially inhibiting such damage and/or regenerating the damaged tissue in a variety of mammals, including humans.

[0040] The foregoing and other objects, features and advantages of the present invention will be made more apparent from the following detailed description of the invention.

Brief Description of the Drawings**[0041]**

5 FIG 1 shows the cardioprotective effects of morphogen (hOP1) in a rat myocardial ischemia-reperfusion model, as evidenced by the smaller loss of myocardial creatine kinase in hOP1-treated rats;

10 FIG 2 shows the effects of 20 µg of morphogen (hOP1 given 24 hours prior to isolation of rat heart on endothelial-dependent vasorelaxation to acetylcholine following induced ischemia-reperfusion injury;

15 FIG 3 shows the effect of morphogen (hOP1) on neutrophil adherence to LTB₄-stimulated mesenteric artery endothelium in neutrophil-activated rats;

20 FIG 4 (A and B) are schematic representations of morphogen inhibition of early mononuclear phagocytic multinuclearization in vivo;

FIG 5 graphs the effect of a morphogen (e.g., OP-1) and a placebo control on mucositic lesion formation; and

25 FIG 6 (A-D) graphs the effects of a morphogen (eg., OP-1, Figs. 6A and 6C) and TGF-β (Fig. 6B and 6D) on collagen (6A and 6B) and hyaluronic acid (6C and 6D) production in primary fibroblast cultures.

Detailed Description of the Invention

25 [0042] It now has been surprisingly discovered that the morphogens defined herein are effective agents in alleviating the tissue destructive effects associated with the body's inflammatory response to tissue injury. In particular, as disclosed herein, the morphogens are capable of alleviating the necrotic tissue effects associated with the ensuing inflammatory responses that occur following an initial tissue injury.

30 [0043] When tissue injury occurs, whether caused by bacteria, trauma, chemicals, heat, or any other phenomenon, the body's inflammatory response is stimulated. In response to signals released from the damaged cells (e.g., cytokines), extravascularization of immune effector cells is induced. Under ordinary circumstances these invading immune effector cells kill the infectious agent and/or infected or damaged cells (through the release of killing substances such as superoxides, peroxins, and other antimicrobial agents stored in granules), remove the dead tissues and organisms (through phagocytosis), release various biological response modifiers that promote rapid healing and covering of the wound (quite often resulting in the formation of fibrotic scar tissue), and then, after the area is successfully healed, exit from the site of the initial insult. Once the site is perceived to be normal, the local release of inflammatory cytokines ceases and the display of adhesion molecules on the vessel endothelium returns to basal levels. In some cases, however, the zeal of these interacting signals and cellular systems, which are designed to capture and contain very rapidly multiplying infectious agents, act to the detriment of the body, killing additional, otherwise healthy, surrounding tissue. This additional unnecessary tissue death further compromises organ function and sometimes results in death of the individual. In addition, the resulting scar tissue that often forms can interfere with normal tissue function as occurs, for example, in idiopathic pulmonary fibrosis, IBD and organ cirrhosis.

35 [0044] The vascular endothelium constitutes the first barrier between circulating immune effector cells and extravascular tissues. Extravasation of these circulating cells requires that they bind to the vascular endothelial cells, cross the basement membrane, and enter insulted tissues e.g., by phagocytosis or protease-mediated extracellular matrix degradation. Without being limited to a particular theory, it is believed that the morphogens of this invention may modulate the inflammatory response in part by modulating the attachment of immune effector cells to the luminal side of the endothelium of blood vessels at or near sites of tissue damage and/or inflammatory lesions. Because the method reduces or prevents the attachment of immune effector cells at these sites, it also prevents the subsequent release of tissue destructive agents by these same immune effector cells at sites of tissue damage and/or inflammatory lesions.

40 [0045] Because attachment of immune effector cells to the endothelium must precede their extravascularization, the method also prevents the initial or continued entry of these cells into extravascular sites of tissue destruction or ongoing inflammatory lesions. Therefore, the invention not only finds utility in a method to reduce or prevent the immune cell-mediated cellular destruction at extravascular sites of recent tissue destruction, but also finds utility in a method to prevent or reduce the continued entry of immune effector cells into extravascular sites of ongoing inflammatory cascades. As will be appreciated by those skilled in the art, the morphogens of this invention also may be contemplated in mechanisms for disrupting the functional interaction of immune effector cells with endothelium where the adhesion molecules are induced by means other than in response to tissue injury.

55 [0046] One source of tissue injury is induced by cell exposure to toxic oxygen concentrations, such as ischemic-

reperfusion tissue injury (oxygen deprivation), and following hyperoxia injury (lethally high oxygen concentrations). Accordingly, the present invention finds utility in a method for alleviating the tissue damage induced by ischemic-reperfusion injury or hyperoxia-induced injury comprising the step of administering to the afflicted individual a therapeutic amount of a morphogen prior to, during, or after damage to the affected tissue. Where the toxic oxygen concentrations may be deliberately induced, as by a surgical or clinical procedure, the morphogen preferably is administered prior to induction.

[0046] In addition, the morphogens described herein, in contrast to fibrogenic growth factors such as TGF- β , stimulate tissue morphogenesis and do not stimulate fibrosis or scar tissue formation (see Example 9, below.) Accordingly, in addition to inhibiting the tissue destructive effects associated with the inflammatory response, the morphogens further enhance the viability of damaged tissue and/or organs by stimulating the regeneration of the damaged tissue and preventing fibrogenesis.

[0047] The morphogens described herein also can inhibit epithelial cell proliferation (see Example 10, below.) This activity of the morphogens also may be particularly useful in the treatment of psoriasis and other inflammatory diseases that involve epithelial cell populations.

[0048] Provided below are detailed descriptions of suitable morphogens useful in the invention, as well as methods for their administration and application, and numerous, nonlimiting examples which 1) illustrate the suitability of the morphogens described herein as therapeutic agents for protecting tissue from the tissue destructive effects associated with the body's inflammatory response; and 2) provide assays with which to test candidate morphogens for their efficacy.

I. Useful Morphogens

[0049] As defined herein a protein is morphogenic if it is capable of inducing the developmental cascade of cellular and molecular events that culminate in the formation of new, organ-specific tissue and comprises at least the conserved C-terminal six cysteine skeleton or its functional equivalent (see supra). Specifically, the morphogens generally are capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. Details of how the morphogens useful in the invention first were identified, as well as a description on how to make, use and test them for morphogenic activity are disclosed in USSN 667,274, filed March 11, 1991 and USSN 752,764, filed August 30, 1991. As disclosed therein, the morphogens may be purified from naturally-sourced material or recombinantly produced from prokaryotic or eucaryotic host cells, using the genetic sequences disclosed therein. Alternatively, novel morphogenic sequences may be identified following the procedures disclosed therein.

[0050] Particularly useful proteins include those which comprise the naturally derived sequences disclosed in Table II. Other useful sequences include biosynthetic constructs such as those disclosed in U.S. Pat. 5,011,691 (e.g., COP-1, COP-3, COP-4, COP-5, COP-7, and COP-16).

[0051] The morphogens useful in the invention also can be described by any of the 6 generic sequences described herein (Generic Sequences 1, 2, 3, 4, 5 and 6). Generic sequences 1 and 2 also may include, at their N-terminus, the sequence

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)

40 1

5

[0052] Table II, set forth below, compares the amino acid sequences of the active regions of native proteins that have been identified as morphogens, including human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-23), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), BMP3 (Seq. ID No. 26), DPP (from *Drosophila*, Seq. ID No. 11), Vgl (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), GDF-1 (from mouse, Seq. ID Nos. 14, 32 and 33), 60A protein (from *Drosophila*, Seq. ID Nos. 24 and 25), BMP5 (Seq. ID No. 27) and BMP6 (Seq. ID No. 28). The sequences are aligned essentially following the method of Needleman et al. (1970) *J. Mol. Biol.*, 48:443-453, calculated using the Align Program (DNAstar, Inc.) In the table, three dots indicates that the amino acid in that position is the same as the amino acid in hOP-1. Three dashes indicates that no amino acid is present in that position, and are included for purposes of illustrating homologies. For example, amino acid residue 60 of CBMP-2A and CBMP-2B is "missing". Of course, both these amino acid sequences in this region comprise Asn-Ser (residues 58, 59), with CBMP-2A then comprising Lys and Ile, whereas CBMP-2B comprises Ser and Ile.

TABLE II

5	hOP-1	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
	mOP-1
	hOP-2	...	Arg	Arg
10	mOP-2	...	Arg	Arg
	DPP	...	Arg	Arg	...	Ser
	Vgl	Lys	Arg	His
15	Vgr-1	Gly
	CBMP-2A	Arg	...	Pro
	CBMP-2B	...	Arg	Arg	...	Ser
20	BMP3	...	Ala	Arg	Arg	Tyr	...	Lys	...
	GDF-1	...	Arg	Ala	Arg	Arg
	60A	...	Gln	Met	Glu	Thr
25	BMP5
	BMP6	...	Arg
		1				5			

30	hOP-1	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
	mOP-1
	hOP-2	Gln	Leu	...
	mOP-2	Ser	Leu	...
35	DPP	Asp	...	Ser	...	Val	Asp	...
	Vgl	Glu	...	Lys	...	Val	Asn
	Vgr-1	Gln	...	Val
40	CBMP-2A	Asp	...	Ser	...	Val	Asn	...
	CBMP-2B	Asp	...	Ser	...	Val	Asn	...
	BMP3	Asp	...	Ala	...	Ile	Ser	Glu
45	GDF-1	Glu	Val	His	Arg
	60A	Asp	...	Lys	His	...
	BMP5
50	BMP6	Gln
		10					15			

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	hOP-1	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
5	mOP-1
	hOP-2	...	Val	Gln	Ser
	mOP-2	...	Val	Gln	Ser
	DPP	Val	Leu	Asp
10	Vgl	...	Val	Gln	Met
	Vgr-1	Lys
	CBMP-2A	Val	Pro	His
	CBMP-2B	Val	Pro	Gln
15	BMP3	Ser	...	Lys	Ser	Phe	Asp
	GDF-1	...	Val	Arg	...	Phe	Leu
	60A	Gly
20	BMP5
	BMP6	Lys
					20				25	
25	hOP-1	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	mOP-1
	hOP-2	Ser
30	mOP-2
	DPP	His	...	Lys	...	Pro
	Vgl	...	Asn	Tyr	Pro
35	Vgr-1	...	Asn	Asp	Ser
	CBMP-2A	...	Phe	His	...	Glu	...	Pro
	CBMP-2B	...	Phe	His	...	Asp	...	Pro
40	BMP3	Ser	...	Ala	...	Gln
	GDF-1	...	Asn	Gln	...	Gln
	60A	...	Phe	Ser	Asn
	BMP5	...	Phe	Asp	Ser
45	BMP6	...	Asn	Asp	Ser
					30				35	
50	hOP-1	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
	mOP-1

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	hOP-2	Asp	...	Cys
	mOP-2	Asp	...	Cys
5	DPP	Ala	Asp	His	Phe	...	Ser
	Vgl	Tyr	Thr	Glu	Ile	Leu	...	Gly
	Vgr-1	Ala	His
10	CBMP-2A	Ala	Asp	His	Leu	...	Ser
	CBMP-2B	Ala	Asp	His	Leu	...	Ser
	GDF-1	Leu	...	Val	Ala	Leu	Ser	Gly	Ser**	...
	BMP3	Met	Pro	Lys	Ser	Leu	Lys	Pro
15	60A	Ala	His
	BMP5	Ala	His	Met
	BMP6	Ala	His	Met
						40				
20										
	hOP-1	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
	mOP-1
25	hOP-2	Leu	...	Ser	...
	mOP-2	Leu	...	Ser	...
	DPP	Val
	Vgl	Ser	Leu
30	Vgr-1
	CBMP-2A
	CBMP-2B
35	BMP3	Ser	Thr	Ile	...	Ser	Ile
	GDF-1	Leu	Val	Leu	Arg	Ala	...
	60A
	BMP5
40	BMP6
			45				50			
45										
	hOP-1	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
	mOP-1	Asp
50	hOP-2	...	His	Leu	Met	Lys	...	Asn	Ala	...
	mOP-2	...	His	Leu	Met	Lys	...	Asp	Val	...

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	DPP	...	Asn	Asn	Asn	Gly	Lys	...
	Vgl	Ser	...	Glu	Asp	Ile
5	Vgr-1	Val	Met	Tyr	...
	CBMP-2A	...	Asn	Ser	Val	...	Ser	---	Lys	Ile
	CBMP-2B	...	Asn	Ser	Val	...	Ser	---	Ser	Ile
10	BMP3	...	Arg	Ala**	Gly	Val	Val	Pro	Gly	Ile
	GDF-1	Met	...	Ala	Ala	Ala	...	Gly	Ala	Ala
	60A	Leu	Leu	Glu	...	Lys	Lys	...
	BMP5	Leu	Met	Phe	...	Asp	His	...
15	BMP6	Leu	Met	Tyr	...
								55		60
20	hOP-1	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	mOP-1
	hOP-2	Ala	Lys
25	mOP-2	Ala	Lys
	DPP	Ala	Val
	Vgl	...	Leu	Val	Lys
30	Vgr-1	Lys
	CBMP-2A	Ala	Val	Glu
	CBMP-2B	Ala	Val	Glu
	BMP3	...	Glu	Val	...	Glu	Lys
35	GDF-1	Asp	Leu	Val	...	Ala	Arg
	60A	Arg
	BMP5	Lys
	BMP6	Lys
40							65		70	
	hOP-1	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
45	mOP-1
	hOP-2	...	Ser	...	Thr	Tyr
	mOP-2	...	Ser	...	Thr	Tyr
50	Vgl	Met	Ser	Pro	Met	...	Phe	Tyr
	Vgr-1	Val

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	DPP	...	Asp	Ser	Val	Ala	Met	Leu
5	CBMP-2A	...	Ser	Met	Leu
	CBMP-2B	...	Ser	Met	Leu
	BMP3	Met	Ser	Ser	Leu	...	Ile	...	Phe	Tyr
10	GDF-1	...	Ser	Pro	Phe	...
	60A	...	Gly	...	Leu	Pro	His
	BMP5
	BMP6
15					75					80
	hOP-1	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
20	mOP-1
	hOP-2	...	Ser	...	Asn	Arg
	mOP-2	...	Ser	...	Asn	Arg
	DPP	Asn	...	Gln	...	Thr	...	Val
25	Vgl	...	Asn	Asn	Asp	Val	...	Arg
	Vgr-1	Asn
	CBMP-2A	...	Glu	Asn	Glu	Lys	...	Val
	CBMP-2B	...	Glu	Tyr	Asp	Lys	...	Val
30	BMP3	...	Glu	Asn	Lys	Val
	GDF-1	...	Asn	...	Asp	Val	...	Arg
	60A	Leu	Asn	Asp	Glu	Asn
35	BMP5
	BMP6	Asn
					85					
40	hOP-1	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	
	mOP-1
45	hOP-2	...	His	Lys	
	mOP-2	...	His	Lys	
	DPP	Asn	...	Gln	Glu	...	Thr	...	Val	
50	Vgl	His	...	Glu	Ala	...	Asp	
	Vgr-1
	CBMP-2A	Asn	...	Gln	Asp	Glu	

55

	CBMP-2B	Asn	...	Gln	Glu	Glu
5	BMP3	Val	...	Pro	Thr	...	Glu
	GDF-1	Gln	...	Glu	Asp	Asp
	60A	Ile	...	Lys
	BMP5
10	BMP6	Trp
			90				95		
15	hOP-1	Ala	Cys	Gly	Cys	His			
	mOP-1			
	hOP-2			
20	mOP-2			
	DPP	Gly	Arg			
	Vgl	Glu	Arg			
25	Vgr-1			
	CBMP-2A	Gly	Arg			
	CBMP-2B	Gly	Arg			
	BMP3	Ser	...	Ala	...	Arg			
30	GDF-1	Glu	Arg			
	60A	Ser			
	BMP5	Ser			
35	BMP6			
			100						

**Between residues 56 and 57 of BMP3 is a Val residue;

between residues 43 and 44 of GDF-1 lies

the amino acid sequence Gly-Gly-Pro-Pro.

[0053] The currently most preferred protein sequences useful as morphogens in this invention include the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). In addition, the most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the Drosophila 60A protein. Accordingly, in still another preferred aspect, the invention includes morphogens comprising species of polypeptide chains having the generic amino acid sequence referred to herein as "OPX", which defines the seven cysteine skeleton and accommodates the identities between the various identified mouse and human OP1 and OP2 proteins. OPX is presented in Seq. ID No. 29. As described therein, each Xaa at a given position independently is selected from the residues occurring at the corresponding position in the C-terminal sequence of mouse or human OP1 or OP2 (see Seq. ID Nos. 5-8 and/or Seq. ID Nos. 16-23).

II. Formulations and Methods for Administering Therapeutic Agents

[0054] The morphogens may be provided to an individual by any suitable means, preferably directly (e.g., locally, as by injection or topical administration to a tissue locus) or systemically (e.g., parenterally or orally). Where the morphogen is to be provided parenterally, such as by intravenous, subcutaneous, intramuscular, intraorbital, ophthalmic, intraventricular, intracranial, intracapsular, intraspinal, intracisternal, intraperitoneal, buccal, rectal, vaginal, intranasal or by

aerosol administration, the morphogen preferably comprises part of an aqueous solution. The solution is physiologically acceptable so that in addition to delivery of the desired morphogen to the patient, the solution does not otherwise adversely affect the patient's electrolyte and volume balance. The aqueous medium for the morphogen thus may comprise normal physiologic saline (9.85% NaCl, 0.15M), pH 7-7.4. The aqueous solution containing the morphogen can be made, for example, by dissolving the protein in 50% ethanol containing acetonitrile in 0.1% trifluoroacetic acid (TFA) or 0.1% HCl, or equivalent solvents. One volume of the resultant solution then is added, for example, to ten volumes of phosphate buffered saline (PBS), which further may include 0.1-0.2% human serum albumin (HSA). The resultant solution preferably is vortexed extensively. If desired, a given morphogen may be made more soluble by association with a suitable molecule. For example, association of the mature dimer with the pro domain of the morphogen keeps the morphogen soluble in physiological buffers. In fact, the endogenous protein is thought to be transported in this form. Another molecule capable of enhancing solubility and particularly useful for oral administrations, is casein. For example, addition of 0.2% casein increases solubility of the mature active form of OP-1 by 80%. Other components found in milk and/or various serum proteins also may be useful.

[0055] Useful solutions for parenteral administration may be prepared by any of the methods well known in the pharmaceutical art, described, for example, in *Remington's Pharmaceutical Sciences* (Gennaro, A., ed.), Mack Pub., 1990. Formulations may include, for example, polyalkylene glycols such as polyethylene glycol, oils of vegetable origin, hydrogenated naphthalenes, and the like. Formulations for direct administration, in particular, may include glycerol and other compositions of high viscosity to help maintain the morphogen at the desired locus. Biocompatible, preferably bioresorbable, polymers, including, for example, hyaluronic acid, collagen, tricalcium phosphate, polybutyrate, lactide and glycolide polymers, and lactide/glycolide copolymers, may be useful excipients to control the release of the morphogen *in vivo*. Other potentially useful parenteral delivery systems for these morphogens include ethylene-vinyl acetate copolymer particles, osmotic pumps, implantable infusion systems, and liposomes. Formulations for inhalation administration contain as excipients, for example, lactose, or may be aqueous solutions containing, for example, polyoxyethylene-9-lauryl ether, glycocholate and deoxycholate, or oily solutions for administration in the form of nasal drops, or as a gel to be applied intranasally. Formulations for parenteral administration may also include glycocholate for buccal administration, methoxysalicylate for rectal administration, or cutric acid for vaginal administration.

[0056] Suppositories for rectal administration also may be prepared by mixing the morphogen or morphogen-stimulating agent with a non-irritating excipient such as cocoa butter or other compositions which are solid at room temperature and liquid at body temperatures.

[0057] Formulations for topical administration to the skin surface may be prepared by dispersing the morphogen or morphogen-stimulating agent with a dermally acceptable carrier such as a lotion, cream, ointment or soap. Particularly useful are carriers capable of forming a film or layer over the skin to localize application and inhibit removal. For topical administration to internal tissue surfaces, the morphogen may be dispersed in a liquid tissue adhesive or other substance known to enhance adsorption to a tissue surface. For example, hydroxypropylcellulose or fibrinogen/thrombin solutions may be used to advantage. Alternatively, tissue-coating solutions, such as pectin-containing formulations, may be used.

[0058] Alternatively, the morphogens described herein may be administered orally. Oral administration of proteins as therapeutics generally is not practiced as most proteins are readily degraded by digestive enzymes and acids in the mammalian digestive system before they can be absorbed into the bloodstream. However, the morphogens described herein typically are acid stable and protease-resistant (see, for example, U.S. Pat.No. 4,968,590.) In addition, at least one morphogen, OP-1, has been identified in mammary gland extract, colostrum and 57-day milk. Moreover, the OP-1 purified from mammary gland extract is morphogenically active. Specifically, this protein induces endochondral bone formation in mammals when implanted subcutaneously in association with a suitable matrix material, using a standard *in vivo* bone assay, such as is disclosed in U.S. Pat.No. 4,968,590. Moreover, the morphogen also is detected in the bloodstream. Finally, soluble form morphogen, e.g., mature morphogen associated with the pro domain, is morphogenically active. These findings indicate that oral and parenteral administration are viable means for administering morphogens to an individual. In addition, while the mature forms of certain morphogens described herein typically are sparingly soluble, the morphogen form found in milk (and mammary gland extract and colostrum) is readily soluble, probably by association of the mature, morphogenically active form with part or all of the pro domain of the intact sequence and/or by association with one or more milk components. Accordingly, the compounds provided herein also may be associated with molecules capable of enhancing their solubility *in vitro* or *in vivo*.

[0059] Where the morphogen or morphogen-stimulating agent comprises part of a tissue or organ preservation solution, any commercially available preservation solution may be used to advantage. For example, useful solutions known in the art include Collins solution, Wisconsin solution, Belzer solution, Eurocollins solution and lactated Ringer's solution. Generally, an organ preservation solution usually possesses one or more of the following properties: (a) an osmotic pressure substantially equal to that of the inside of a mammalian cell,(solutions typically are hyperosmolar and have K⁺ and/or Mg⁺⁺ ions present in an amount sufficient to produce an osmotic pressure slightly higher than the inside of a mammalian cell; (b) the solution typically is capable of maintaining substantially normal ATP levels in the

cells; and (c) the solution usually allows optimum maintenance of glucose metabolism in the cells. Organ preservation solutions also may contain anticoagulants, energy sources such as glucose, fructose and other sugars, metabolites, heavy metal chelators, glycerol and other materials of high viscosity to enhance survival at low temperatures, free oxygen radical inhibiting agents and a pH indicator. A detailed description of preservation solutions and useful components may be found, for example, in US Patent No. 5,002,965.

[0060] The compounds provided herein also may be associated with molecules capable of targeting the morphogen or morphogen-stimulating agent to the desired tissue. For example, an antibody, antibody fragment, or other binding protein that interacts specifically with a surface molecule on cells of the desired tissue, may be used. Useful targeting molecules may be designed, for example, using the single chain binding site technology disclosed, for example, in U. S. Pat. No. 5,091,513.

[0061] As described above, the morphogens provided herein share significant sequence homology in the C-terminal active domains. By contrast, the sequences typically diverge significantly in the sequences which define the pro domain. Accordingly, the pro domain is thought to be morphogen-specific. As described above, it is also known that the various morphogens identified to date are differentially expressed in the different tissues. Accordingly, without being limited to any given theory, it is likely that, under natural conditions in the body, selected morphogens typically act on a given tissue. Accordingly, part or all of the pro domains which have been identified associated with the active form of the morphogen in solution, may serve as targeting molecules for the morphogens described herein. For example, the pro domains may interact specifically with one or more molecules at the target tissue to direct the morphogen associated with the pro domain to that tissue. Accordingly, another useful targeting molecule for targeting morphogen to a tissue of interest is part or all of a morphogen pro domain. For example, part or all of the pro domain of GDF-1 may be used to target a morphogen to nerve tissue. Alternatively, part or all of the pro domain of OP-1 or CBMP2 may be used to target a morphogen to bone tissue, both of which proteins are found naturally associated with bone tissue.

[0062] The morphogens described herein are useful for providing neuroprotective effects to alleviate neural pathway damage associated with the body's immune/inflammatory response to an initial injury to nerve tissue. As used herein, a "neural pathway" describes a nerve circuit for the passage of electric signals from a source to a target cell site and includes both the central nervous system (CNS) and peripheral nervous system (PNS). The pathway includes the neurons through which the electric impulse is transported, including groups of interconnecting neurons, the nerve fibers formed by bundled neuronal axons, and the glial cells surrounding and associated with the neurons. An inflammatory response to nerve tissue injury may follow trauma to nerve tissue, caused, for example, by an autoimmune (including autoantibody) dysfunction, neoplastic lesion, infection, chemical or mechanical trauma, or other disease. An exemplary nerve-related inflammatory disease is multiple sclerosis. Neural pathway damage also can result from a reduction or interruption, e.g., occlusion, of a neural blood supply, as in an embolic stroke, (e.g. ischemia or hypoxia-induced injury), or by other trauma to the nerve or surrounding material. In addition, at least part of the damage associated with a number of primary brain tumors also appears to be immunologically related. Application of the morphogen directly to the cells to be treated, or providing the morphogen to the mammal systemically, for example, intravenously or indirectly by oral administration, may be used to alleviate and/or inhibit the immunologically related response to a neural injury. Alternatively, administration of an agent capable of stimulating morphogen expression and/or secretion *in vivo*, preferably at the site of injury, also may be used. Where the injury is to be induced, as during surgery or other aggressive clinical treatment, the morphogen or agent may be provided prior to induction of the injury to provide a neuroprotective effect to the nerve tissue at risk.

[0063] Where the morphogen is intended for use as a therapeutic to alleviate tissue damage associated with an immune/inflammatory condition of the CNS, an additional problem must be addressed: overcoming the so-called "blood-brain barrier", the brain capillary wall structure that effectively screens out all but selected categories of molecules present in the blood, preventing their passage into the brain. The blood-brain barrier may be bypassed effectively by direct infusion of the morphogen or morphogen-stimulating agent into the brain. Alternatively, the morphogen or morphogen-stimulating agent may be modified to enhance its transport across the blood-brain barrier. For example, truncated forms of the morphogen or a morphogen-stimulating agent may be most successful. Alternatively, the morphogen or morphogen-stimulating agent may be modified to render it more lipophilic, or it may be conjugated to another molecule which is naturally transported across the barrier, using standard means known to those skilled in the art, as, for example, described in Pardridge, *Endocrine Reviews* 7:314-330 (1986) and U.S. Pat. No. 4,801,575.

[0064] Finally, the morphogens provided herein may be administered alone or in combination with other molecules known to be beneficial in the treatment compositions and methods described herein, including, but not limited to anticoagulants, free oxygen radical inhibiting agents, salicylic acid, vitamin D, and other anti-inflammatory agents. Psoriasis treatments also may include ultra-violet light treatment, zinc oxide and retinoids.

[0065] The compounds provided herein can be formulated into pharmaceutical compositions by admixture with pharmaceutically acceptable nontoxic excipients and carriers. As noted above, such compositions may be prepared for parenteral administration, particularly in the form of liquid solutions or suspensions; for oral administration, particularly in the form of tablets or capsules; or intranasally, particularly in the form of powders, nasal drops, or aerosols.

[0066] The compositions can be formulated for parenteral or oral administration to humans or other mammals in therapeutically effective amounts, e.g., amounts which provide appropriate concentrations for a time sufficient to alleviate the tissue destructive effects associated with the inflammatory response, including protecting tissue in anticipation of tissue damage.

5 [0067] As will be appreciated by those skilled in the art, the concentration of the compounds described in a therapeutic composition will vary depending upon a number of factors, including the dosage of the drug to be administered, the chemical characteristics (e.g., hydrophobicity) of the compounds employed, and the route of administration. The preferred dosage of drug to be administered also is likely to depend on such variables as the type and extent of progression of the tissue damage, the overall health status of the particular patient, the relative biological efficacy of the compound selected, the formulation of the compound excipients, and its route of administration. In general terms, the compounds of this invention may be provided in an aqueous physiological buffer solution containing about 0.001% to 10% w/v compound for parenteral administration. Typical dose ranges are from about 10 ng/kg to about 1 g/kg of body weight per day; a preferred dose range is from about 0.1 µg/kg to 100 mg/kg of body weight per day. Optimally, the morphogen dosage given is between 0.1-100 µg of protein per kilogram weight of the patient. No obvious morphogen induced pathological lesions are induced when mature morphogen (e.g., OP-1,20 µg) is administered daily to normal growing rats for 21 consecutive days. Moreover, 10 µg systemic injections of morphogen (e.g., OP-1) injected daily for 10 days into normal newborn mice does not produce any gross abnormalities.

10 [0068] In administering morphogens systemically, preferably a large volume loading dose is used at the start of the treatment. The treatment then is continued with a maintenance dose. Further administration then can be determined by monitoring at intervals the levels of the morphogen in the blood.

15 [0069] Where tissue injury is induced deliberately as part of, for example, a surgical procedure, the morphogen preferably is provided just prior to, or concomitant with induction of the trauma. Preferably, the morphogen is administered prophylactically in a surgical setting.

20 [0070] Alternatively, an effective amount of an agent capable of stimulating endogenous morphogen levels may be administered by any of the routes described above. For example, an agent capable of stimulating morphogen production and/or secretion from cells of affected tissue and/or transplant tissue may be provided to a mammal, e.g., by direct administration of the agent to the tissue to be treated. A method for identifying and testing agents capable of modulating the levels of endogenous morphogens in a given tissue is described generally herein in Example 15, and in detail in copending USSN 752,859, filed August 30, 1991. Briefly, candidate compounds can be identified and tested by incubating the compound *in vitro* with a test tissue or cells thereof, for a time sufficient to allow the compound to affect the production, i.e., the expression and/or secretion, of a morphogen produced by the cells of that tissue.

25 [0071] For purposes of the present invention, the above-described morphogens effective in alleviating tissue damage associated with ischemic-reperfusion injury are administered prior to or during the restoration of oxygen (e.g., restoration of blood flow, reperfusion.) Where treatment is to follow an existing injury, the therapeutic agent preferably is administered as an intravenous infusion provided acutely after the hypoxic or ischemic condition occurs. For example, the therapeutic agent can be administered by intravenous infusion immediately after a cerebral infarction, a myocardial infarction, asphyxia, or a cardiopulmonary arrest. Where ischemia or hypoxia injury is deliberately and/or unavoidably induced as part of, for example, a surgical procedure where circulation to an organ or organ system is deliberately and/or transiently interrupted, e.g., in carotid enterectomy, coronary artery bypass, grafting, organ transplanting, fibrinolytic therapy, etc., the therapeutic agent preferably is provided just prior to, or concomitant with, reduction of oxygen to the tissue. Preferably, the morphogen is administered prophylactically in a surgical setting.

30 [0072] Similarly, where hyperoxia-induced injury already has occurred, the morphogen is administered upon diagnosis. Where hyperoxia injury may be induced as, for example, during treatment of prematurely newborn babies, or patients suffering from pulmonary diseases such as emphysema, the therapeutic agent preferably is administered prior to administration of oxygen e.g., prophylactically.

III. Examples

Example 1. Identification of Morphogen-Expressing Tissue

35 [0073] Determining the tissue distribution of morphogens may be used to identify different morphogens expressed in a given tissue, as well as to identify new, related morphogens. Tissue distribution also may be used to identify useful morphogen-producing tissue for use in screening and identifying candidate morphogen-stimulating agents. The morphogens (or their mRNA transcripts) readily are identified in different tissues using standard methodologies and minor modifications thereof in tissues where expression may be low. For example, protein distribution may be determined using standard Western blot analysis or immunofluorescent techniques, and antibodies specific to the morphogen or morphogens of interest. Similarly, the distribution of morphogen transcripts may be determined using standard Northern hybridization protocols and transcript-specific probes.

[0074] Any probe capable of hybridizing specifically to a transcript, and distinguishing the transcript of interest from other, related transcripts may be used. Because the morphogens described herein share such high sequence homology in their active, C-terminal domains, the tissue distribution of a specific morphogen transcript may best be determined using a probe specific for the pro region of the immature protein and/or the N-terminal region of the mature protein.

5 Another useful sequence is the 3' non-coding region flanking and immediately following the stop codon. These portions of the sequence vary substantially among the morphogens of this invention, and accordingly, are specific for each protein. For example, a particularly useful Vgr-1-specific probe sequence is the Pvull-Sacl fragment, a 265 bp fragment encoding both a portion of the untranslated pro region and the N-terminus of the mature sequence (see Lyons et al. (1989) *PNAS* 86:4554-4558 for a description of the cDNA sequence). Similarly, particularly useful mOP-1-specific

10 probe sequences are the BstX1-BglII fragment, a 0.68 Kb sequence that covers approximately two-thirds of the mOP-1 pro region; a StuI-StuI fragment, a 0.2 Kb sequence immediately upstream of the 7-cysteine domain; and the Ear1-PstI fragment, an 0.3 Kb fragment containing a portion of the 3'untranslated sequence (See Seq. ID No. 18, where the pro region is defined essentially by residues 30-291.) Similar approaches may be used, for example, with hOP-1 (Seq. ID No. 16) or human or mouse OP-2 (Seq. ID Nos. 20 and 22.)

15 [0075] Using these morphogen-specific probes, which may be synthetically engineered or obtained from cloned sequences, morphogen transcripts can be identified in mammalian tissue, using standard methodologies well known to those having ordinary skill in the art. Briefly, total RNA is prepared from various adult murine tissues (e.g., liver, kidney, testis, heart, brain, thymus and stomach) by a standard methodology such as by the method of Chomczyaski et al. ((1987) *Anal. Biochem* 162:156-159) and described below. Poly (A)+ RNA is prepared by using oligo (dT)-cellulose

20 chromatography (e.g., Type 7, from Pharmacia LKB Biotechnology, Inc.). Poly (A)+ RNA (generally 15 µg) from each tissue is fractionated on a 1% agarose/formaldehyde gel and transferred onto a Nytran membrane (Schleicher & Schuell). Following the transfer, the membrane is baked at 80°C and the RNA is cross-linked under UV light (generally 30 seconds at 1 mW/cm²). Prior to hybridization, the appropriate probe is denatured by heating. The hybridization is carried out in a lucite cylinder rotating in a roller bottle apparatus at approximately 1 rev/min for approximately 15 hours

25 at 37°C using a hybridization mix of 40% formamide, 5 x Denhardt's, 5 x SSPE, and 0.1% SDS. Following hybridization, the non-specific counts are washed off the filters in 0.1 x SSPE, 0.1% SDS at 50°C.

[0076] Examples demonstrating the tissue distribution of various morphogens, including Vgr-1, OP-1, BMP2, BMP3, BMP4, BMP5, GDF-1, and OP-2 in developing and adult tissue are disclosed in co-pending USSN 752, 764, and in Ozkaynak, et al., (1991) *Biochem. Biophys. Res. Commn.* 179:116-123, and Ozkaynak, et al. (1992) (JBC, in press).

30 Using the general probing methodology described herein, northern blot hybridizations using probes specific for these morphogens to probe brain, spleen, lung, heart, liver and kidney tissue indicate that kidney-related tissue appears to be the primary expression source for OP-1, with brain, heart and lung tissues being secondary sources. OP-1 mRNA also was identified in salivary glands, specifically rat parotid glands, using this probing methodology. Lung tissue appears to be the primary tissue expression source for Vgr-1, BMP5, BMP4 and BMP3. Lower levels of Vgr-1 also are seen in kidney and heart tissue, while the liver appears to be a secondary expression source for BMP5, and the spleen appears to be a secondary expression source for BMP4. GDF-1 appears to be expressed primarily in brain tissue. To date, OP-2 appears to be expressed primarily in early embryonic tissue. Specifically, northern blots of murine embryos and 6-day post-natal animals shows abundant OP2 expression in 8-day embryos. Expression is reduced significantly in 17-day embryos and is not detected in post-natal animals.

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Example 2. Active Morphogens in Body Fluids

[0077] OP-1 expression has been identified in saliva (specifically, the rat parotid gland, see Example 1), human blood serum, and various milk forms, including mammary gland extract, colostrum, and 57-day bovine milk. Moreover, and as described in USSN 923,780, the body fluid-extracted protein is morphogenically active. The discovery that the morphogen naturally is present in milk and saliva, together with the known observation that mature, active OP-1 is acid-stable and protease-resistant, indicate that oral administration is a useful route for therapeutic administration of morphogen to a mammal. Oral administration typically is the preferred mode of delivery for extended or prophylactic therapies. In addition, the identification of morphogen in all milk forms, including colostrum, suggests that the protein may play a significant role in tissue development, including skeletal development, of juveniles.

2.1 Morphogen Detection in Milk

[0078] OP-1 was partially purified from rat mammary gland extract and bovine colostrum and 57 day milk by passing these fluids over a series of chromatography columns: (e.g., cation-exchange, affinity and reverse phase). At each step the eluant was collected in fractions and these were tested for the presence of OP-1 by standard immunoblot. Immunoreactive fractions then were combined and purified further. The final, partially purified product then was examined for the presence of OP-1 by Western blot analysis using OP-1-specific antisera, and tested for in vivo and in vitro

activity.

[0079] OP-1 purified from the different milk sources were characterized by Western blotting using antibodies raised against OP-1 and BMP2. Antibodies were prepared using standard immunology protocols well known in the art, and as described generally in Example 15, below, using full-length *E. coli*-produced OP-1 and BMP2 as the immunogens.

5 In all cases, the purified OP-1 reacted only with the anti-OP-1 antibody, and not with anti-BMP2 antibody.

[0080] The morphogenic activity of OP-1 purified from mammary gland extract was evaluated *in vivo* essentially following the rat model assay described in U.S. Pat. No. 4,968,590. Briefly, a sample was prepared from each OP-1 immunoreactive fraction of the mammary gland extract-derived OP-1 final product by lyophilizing a portion (33%) of the fraction and resuspending the protein in 220 μ l of 50% acetonitrile/0.1% TFA. After vortexing, 25 mg of collagen matrix was added. The samples were lyophilized overnight, and implanted in Long Evans rats (Charles River Laboratories, Wilmington, MA, 28-35 days old). Each fraction was implanted in duplicate. For details of the collagen matrix implantation procedure, see, for example, U.S. Pat. No. 4,968,590. After 12 days, the implants were removed and evaluated for new bone formation by histological observation as described in U.S. Patent No. 4,968,590. In all cases, the immunoreactive fractions were osteogenically active.

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2.2 Morphogen Detection in Serum

[0081] Morphogen may be detected in serum using morphogen-specific antibodies. The assay may be performed using any standard immunoassay, such as Western blot (immunoblot) and the like. Preferably, the assay is performed using an affinity column to which the morphogen-specific antibody is bound and through which the sample serum then is poured, to selectively extract the morphogen of interest. The morphogen then is eluted. A suitable elution buffer may be determined empirically by determining appropriate binding and elution conditions first with a control (e.g., purified, recombinantly-produced morphogen.) Fractions then are tested for the presence of the morphogen by standard immunoblot, and the results confirmed by N-terminal sequencing. Preferably, the affinity column is prepared using monoclonal antibodies. Morphogen concentrations in serum or other fluid samples then may be determined using standard protein quantification techniques, including by spectrophotometric absorbance or by quantitation of conjugated antibody.

[0082] Presented below is a sample protocol for identifying OP-1 in serum. Following this general methodology other morphogens may be detected in body fluids, including serum. The identification of morphogen in serum further indicates that systemic administration is a suitable means for providing therapeutic concentrations of a morphogen to an individual, and that morphogens likely behave systemically as endocrine-like factors. Finally, using this protocol, fluctuations in endogenous morphogen levels can be detected, and these altered levels may be used as an indicator of tissue dysfunction. Alternatively, fluctuations in morphogen levels may be assessed by monitoring morphogen transcription levels, either by standard northern blot analysis as described in Example 1, or by *in situ* hybridization, using a labelled probe capable of hybridizing specifically to morphogen mRNA, and standard RNA hybridization protocols well described in the art and described generally in Example 1.

[0083] OP-1 was detected in human serum using the following assay. A monoclonal antibody raised against mammalian, recombinantly produced OP-1 using standard immunology techniques well described in the art and described generally in Example 15, was immobilized by passing the antibody over an agarose-activated gel (e.g., Affi-Gel™, from Bio-Rad Laboratories, Richmond, CA, prepared following manufacturer's instructions) and used to purify OP-1 from serum. Human serum then was passed over the column and eluted with 3M K-thiocyanate. K-thiocyanate fractions then were dialyzed in 6M urea, 20mM PO₄, pH 7.0, applied to a C8 HPLC column, and eluted with a 20 minute, 25-50% acetonitrile/0.1 % TFA gradient. Mature, recombinantly produced OP-1 homodimers elute between 20-22 minutes. Fractions then were collected and tested for the presence of OP-1 by standard immunoblot using an OP-1 specific antibody as for Example 2.A.

[0084] Administered or endogenous morphogen levels may be monitored in the therapies described herein by comparing the quantity of morphogen present in a body fluid sample with a predetermined reference value, for example, to evaluate the efficiency of a therapeutic protocol, and the like. In addition, fluctuations in the level of endogenous morphogen antibodies may be detected by this method, most likely in serum, using an antibody or other binding protein capable of interacting specifically with the endogenous morphogen antibody. Detected fluctuations in the levels of the morphogen or endogenous antibody may be used, for example, as indicators of a change in tissue status. For example, as damaged tissue is regenerated and the tissue or organ's function returns to "normal" and, in the absence of additional tissue damage, lower doses of morphogen may be required, and a higher level of circulating morphogen antibody may be measured.

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Example 3. Effect of Morphogen after the Onset of the Ischemic Process

[0085] The cardioprotective effect of morphogens following ischemic-reperfusion injury in a mammal can readily be

assessed in a rat model. In this example, morphogen (e.g., OP-1) is administered just prior to the onset of the ischemic process in experimentally-induced myocardial infarcted rats, essentially following the method of Lefer, et al. (1990) *Science* 249:61-64 and (1992) *J. Mol. Cell. Cardiol.* 24: 385-393. Briefly, loss of myocardial tissue function following ischemia and reperfusion is assayed by measuring loss of myocardial creatine kinase activity (CK) and loss of endothelium-dependent vasorelaxation function (see Example 4, below).

[0086] In a first group of ether-anesthetized rats, the left coronary artery was occluded just proximal to the first main branch with a silk ligature to induce a myocardial infarction (MI). The ligature was removed 10 minutes after occlusion to allow for coronary reperfusion. This first group is referred to herein as the "myocardial infarcted" (MI) group. A second group of rats underwent the same procedure except that the coronary artery was not occluded, and thus no myocardial infarction occurred. The second group of rats is referred to herein as the "sham myocardial infarcted group" (SHAM MI).

[0087] The first group of rats, the MI group of rats, further was divided into three sub-groups. 2 μ g of morphogen (OP-1) were injected intravenously into the first sub-group of MI rats 10 minutes after ligature, immediately before reperfusion; into the second sub-group of MI rats 20 μ g of OP-1 were injected intravenously 10 minutes after ligature and immediately before reperfusion; and into the third sub-group of MI rats (control) was injected vehicle only, e.g., 0.9% NaCl, as for the OP-1 treated rats.

[0088] Twenty-four hours later, the hearts were removed from all of the rats and the levels of creatine kinase (CK) from the left ventricle (the infarcted region) and from the interventricular septum (the control nonischemic region) were determined by standard means. By comparing the difference in CK activities in both regions, the amount of CK activity lost from the infarcted region was used as an index of cardiac cellular injury to the infarcted region.

[0089] As shown in Figure 1, the data indicate that morphogens (e.g., OP-1) can provide significant cardioprotective effect when provided to ischemic tissue. In the figure, CK loss is graphed as the difference in specific CK activity between the interventricular septum and the left ventricle.

[0090] The loss of CK activity by the subgroup of MI rats which received 2 μ g of OP-1 just before reperfusion showed some protection as compared with the control MI rats which received injections of vehicle alone, when the levels from both subgroups are measured against, and compared to, the levels obtained for the SHAM MI control. Significant cardioprotection was observed in the subgroup of MI rats which received 20 μ g of OP-1 immediately before reperfusion as compared with the control MI rats which received injections of vehicle alone, when the levels from both subgroups are measured against, and compared to, the levels contained within the SHAM MI control.

[0091] These data indicate that OP-1 offers significant cardiac protection when administered after ischemia and before reperfusion.

[0092] A variation of this example also may be performed providing morphogen to the animal prior to induction of ischemia. The experiments may be performed both in normal and immune-compromised rats to assess the cardioprotective effects of morphogen administered prior to ischemia.

35 Example 4. Vasodilation of Myocardial Infarcted Cardiac Tissue Treated with Morphogen

[0093] Certain vasodilators like acetylcholine (ACh) and adenosine diphosphate (ADP, an immune mediator) exert their vasodilation activity only in the presence of intact endothelium, which is stimulated to release a substance termed endothelium-derived relaxing factor (EDRF). If the endothelium is injured so that EDRF is not released, no vasodilation occurs in response to these endothelium-dependent agents. In contrast, several other vasodilators including nitroglycerine (NTG) and nitroprusside, are endothelium-independent dilators, as they dilate blood vessels directly.

[0094] The present example demonstrates the ability of OP-1 to prevent the loss of cardioendothelium-dependent relaxation (EDR) activity in the coronary microvasculature following reperfusion of ischemic myocardium, and their ability to reduce myocardial injury 24 hours after morphogen treatment. Briefly, 2 or 24 hours after morphogen treatment ischemia-reperfusion injury is induced in isolated rat hearts, the reperfused hearts are vasodilated with either ACh or NTG. In the absence of morphogen treatment, injured tissue should inhibit ACh-induced vasodilation, but not NTG-induced vasodilation. Morphogen treatment is expected to enhance ACh-induced vasodilation in the reperfused hearts.

[0095] Accordingly, 48 adult male Sprague-Dawley rats (250-330 g) were divided into eight groups of 6 rats each. Twelve rats were subjected to sham myocardial infarcts (SHAM MI) as described in Example 3. The hearts of the remaining 36 rats were isolated as follows: one set of twelve rats was injected intravenously with OP-1 24 hours prior to isolation of the heart; another set of rats was injected intravenously with 20 μ g of OP-1 2 hours prior to isolation of the heart; the final group of rats was injected with vehicle only (e.g., 0.9% NaCl.). The rats then were anesthetized with pentobarbital sodium (35 mg/kg, intraperitoneal); their hearts were isolated and perfused by the Langendorff method at a constant flow (15 ml/min) with oxygenated Krebs-Henseleit solution (Aoki et al. (1988) *J. Pharmacol.* 95:35).

[0096] Each group of rats then were divided into two subgroups of six rats each. Twenty minutes before reperfusion, coronary vasodilator response was measured by inducing constriction with 0.05 μ mol U-44619 (9,11-methanoepoxy-prostaglandin H₂) followed by a vasodilating agent 3 minutes later: subgroup one - 15 nmol ACh; subgroup 2 - 15 nmol NTG and the increase in coronary perfusion pressure (CPP) level measured as an indication of vasodilation. When

CPP levels returned to normal, the hearts were subjected to ischemia by reducing coronary infusion to 15% of control flow for 30 minutes, then reestablishing normal flow, i.e., reperfusion, for an additional 20 minutes.

[0097] The vasodilator response then was remeasured by constriction and administration of vasodilating agent as described above.

5 [0098] The results of these experiments are shown in FIG 2. Before the ischemic event, both Ach and NTG gave normal vasorelaxant results in all events. The hearts which received OP-1 24 hours prior to ischemia showed an approximately 70% response to ACh while the hearts which received OP-1 2 hours prior to ischemia showed a 55% response to ACh. The group which received vehicle alone showed a 40% response to ACh. Finally, the control group which was not subjected to ischemia showed an ACh response of approximately 95%. This shows that endothelium-dependent vasodilators exert a reduced vasodilator response following ischemia and reperfusion in the rat heart. Moreover, OP-1 significantly preserved endothelium-dependent dilation when provided 24 hours prior to induction of myocardial ischemia. No defect in vasodilation occurred in response to the direct vasodilator (NTG); NTG-induced vasodilation activities were 95% of initial in hearts subject to ischemia and 100% of initial nonischemic hearts.

10 15 Example 5. Effect of Morphogen on Neutrophil Adherence

20 [0099] The role of neutrophil adherence in endothelium dysfunction and the cardioprotective effects of morphogens in modulating this activity can be assessed using a standard polymorphonuclear neutrophil (PMN) adherence assay such as described in Lefer et al., (1992) *J. Mol. Cell. Cardiol.* 24: 385-393. Briefly, segments of superior mesenteric artery were isolated from rats which had either been treated with morphogen (OP-1, 20 µg) or 0.9% NaCl, 24 h prior to isolation of the artery. The segments were cleaned, cut into transverse rings of 1-2mm in length, and these were subsequently cut open and incubated in K-H solution at 37°C, pH 7.4. Neutrophils were prepared and fluorescently labelled using standard procedures (e.g., leukocytes were isolated from rats essentially following the procedure of Pertroft et. al. (1968) *Exp Cell Res* 50: 355-368, washed in phosphate buffered saline (PBS), purified by gradient centrifugation; and labelled by the method of Yuan et. al. (1990) *Microvasc Res* 40: 218-229..

25 [0100] Labelled neutrophils then were added to open ring baths and activated with 100nM leukotriene B₄ (LTB₄). Rings were incubated for 20 minutes and the number of neutrophils adhering to the endothelial surface then determined visually by fluorescent microscopy.

30 [0101] As shown in Figure 3, unstimulated PMNs (i.e., PMNS alone) added to the baths did not significantly adhere to the vascular endothelium. In rings taken from rats injected with 0.9% NaCl, activation of neutrophils with LTB₄ (100 nM) greatly increased the number of PMNs adherent to the endothelium ($P<0.001$). OP-1 (20 µg administered 24 h prior) significantly inhibited adherence of PMNs activated by LTB₄ ($P<0.01$ from control).

35 Example 6. In Vivo Models for Ischemic-Reperfusion Protection in Lung, Nerve and Renal Tissue.

[0102] Other tissues seriously affected by ischemic-reperfusion injury include neural tissue, renal tissue and lung tissue. The effect of morphogens on alleviating the ischemic-reperfusion injury in these tissues may be assessed using methodologies and models known to those skilled in the art, and disclosed below. Similarly, a methodology also is provided for assessing the tissue-protective effects of a morphogen on damaged lung tissue following hyperoxia injury.

40 [0103] For example, the rabbit embolic stroke model provides a useful method for assessing the effect of morphogens on tissue injury following cerebral ischemia-reperfusion. The protocol disclosed below is essentially that of Phillips et al. (1989) *Annals of Neurology* 25:281-285. Briefly, white New England rabbits (2-3kg) are anesthetized and placed on a respirator. The intracranial circulation then is selectively catheterized by the Seldinger technique. Baseline cerebral angiography then is performed, employing a digital subtraction unit. The distal internal carotid artery or its branches then is selectively embolized with 0.035 ml of 18-hour-aged autologous thrombus. Arterial occlusion is documented by repeat angiography immediately after embolization. After a time sufficient to induce cerebral infarcts (15 minutes or 90 minutes), reperfusion is induced by administering a bolus of a reperfusion agent such as the TPA analogue Fb-FB-CF (e.g., 0.8 mg/kg over 2 minutes).

45 [0104] The effect of morphogen on cerebral infarcts can be assessed by administering varying concentrations of morphogens, e.g., OP1, at different times preceding or following embolization and/or reperfusion. The rabbits are sacrificed 3-14 days post embolization and their brains prepared for neuropathological examination by fixing by immersion in 10% neutral buffered formalin for at least 2 weeks. The brains then are sectioned in a coronal plane at 2-3 mm intervals, numbered and submitted for standard histological processing in paraffin, and the degree of neural tissue necrosis determined visually.

50 [0105] The renal-protective effects of morphogens on renal ischemia-reperfusion injury readily can be assessed using the mouse model disclosed by Ouellette, et al. (1990), *J. Clin. Invest.* 85:766-771. Briefly, renal ischemia is induced surgically in 35-45 days old out-bred Swiss male mice by performing a standard right nephrectomy, and occluding the artery to the left kidney with a microaneurism clamp for 10-30 minutes. Morphogen then may be provided

parentally, at various times prior to or following occlusion and/or reperfusion. The effects of morphogen then may be assessed by biological evaluation and histological evaluation using standard techniques well known in the art.

[0106] The tissue protective effects of morphogen on tissue exposed to lethally high oxygen concentrations may be assessed by the following procedure. Adult rats (275-300 gms) first are provided with morphogen (e.g., hOP1) or vehicle only, and then are exposed to 96-98% oxygen essentially as described by Rinaldo et al (1983) *Am. Rev. Respir. Dis.* 130:1065, to induce hyperoxia. Animals are housed in plastic cages (38 cm x 48 xm x 21 cm). A cage containing 4-5 animals is placed in a 75 liter water-sealed plexiglass chamber. An atmosphere of 96-98% oxygen then is maintained by delivery of O₂ gas (liquid O₂). Gas flow through the chamber is adjusted to maintain at least 10 air changes/hr., temperature at 22 ± 1°C, minimal levels of condensation within the cage, and carbon dioxide concentration of < 0.5% as measured with a mass spectrophotometric medical gas analyzer.

[0107] At the end of 72 hours all survivors are observed at room air for 1.5 hours and at longer time periods to assess degree of respiratory distress and cyanosis induced by the initial insult and subsequent immune cell-mediated damage. The number of survivors at the end of the challenge is recorded and the treated groups compared with the untreated control group by chi-square test of proportions. Several of the surviving animals for each group are randomly chosen for histological processing of lung tissue.

[0108] Lung tissue for histological processing is fixed by infusion of 10% buffered formalin through a tracheal cannula at a constant pressure of 20 cm H₂O. After fixation for 24-48 hours, sections from each lobe are cut and subsequently stained with hematoxylin and eosin. Coded slides then are examined, preferably in a double-blind fashion for evidence of pathological changes such as edema, interstitial cellularity, and inflammatory response.

Example 7. Morphogen Inhibition of Cellular and Humoral Inflammatory Response

[0109] Morphogens described herein inhibit multinucleation of mononuclear phagocytic cells under conditions where these cells normally would be activated, e.g., in response to a tissue injury or the presence of a foreign substance. For example, in the absence of morphogen, an implanted substrate material (e.g., implanted subcutaneously) composed of, for example, mineralized bone, a ceramic such as titanium oxide or any other substrate that provokes multinucleated giant cell formation, rapidly becomes surrounded by multinucleated giant cells, e.g., activated phagocytes stimulated to respond and destroy the foreign object. In the presence of morphogen however, the recruited cells remain in their mononuclear precursor form and the matrix material is undisturbed. Figure 4 illustrates this effect of morphogens, in a schematic representation of histology results of a titanium oxide substrate implanted subcutaneously. In the figure, "mg" means mononuclear giant cells and "ob" means osteoblasts. The substrate represented in Fig. 4B was implanted together with morphogen (OP-1) and newly formed osteoblasts are evident surrounding the substrate. By contrast, the substrate represented in Fig. 4A was implanted without morphogen and extensive multinucleated giant cell formation is evident surrounding the substrate. Accordingly, the morphogens' effect in inhibiting excessive bone mass loss in a mammal also may include inhibiting activation of these cells.

[0110] In addition, the morphogens described herein also suppress antibody production stimulated in response to a foreign antigen in a mammal. Specifically, when bovine bone collagen matrix alone was implanted in a bony site in a rat, a standard antibody response to the collagen is stimulated in the rat as determined by standard anti-bovine collagen ELISA experiments performed on blood samples taken at four week intervals following implantation (e.g., between 12 and 20 weeks.) Serum anti-collagen antibody titers, measured by ELISA essentially following the procedure described by Nagler-Anderson et al, (1986) *PNAS* 83:7443-7446, increased consistently throughout the experiment. However, when the matrix was implanted together with a morphogen (e.g., OP-1, dispersed in the matrix and adsorbed thereto, essentially as described in U.S. Pat. No. 4,968,590) anti-bovine collagen antibody production was suppressed significantly. This ability of morphogen to suppress the humoral response is further evidence of morphogen utility in alleviating tissue damage associated with autoimmune diseases, including autoantibody diseases, such as rheumatoid arthritis.

Example 8. Morphogen protection of Gastrointestinal Tract Mucosa from Ulceration and Inflammation

[0111] Oral mucositis is a gastrointestinal tract inflammatory disease which involves ulcerations of the mouth mucosa as a consequence of, e.g., radiation therapy or chemotherapy. While not typically a chronic disease, the tissue destructive effects of oral mucositis mirror those of chronic inflammatory diseases such as IBD. The example below demonstrates morphogen efficacy in protecting the oral mucosa from oral mucositis in a hamster model, including both inhibiting inflammatory ulceration and enhancing regeneration of ulcerated tissue. Details of the protocol can be found in Sonis, et al., (1990) *Oral Surg. Oral Med. Oral Pathol* 69: 437-443. Based on these data, the morphogens described herein should be efficacious in treating chronic inflammatory diseases including IBD, arthritis, psoriasis and psoriatic arthritis, multiple sclerosis, and the like.

[0112] Golden syrian hamsters (6-8 wks old, Charles River Laboratories, Wilmington, MA) were divided into 3 test groups: Group 1, a placebo (e.g., saline) control, and a morphogen low dose group (100 ng) and a morphogen high

dose group (1 µg), Groups 2 and 3, respectively. Morphogen dosages were provided in 30% ethanol. Each group contained 12 animals.

[0113] Beginning on day 0 and continuing through day 5, Groups 2 and 3 received twice daily morphogen applications. On day 3, all groups began the mucositis-induction procedure. 5-fluorouracil (60 mg/kg) was injected intraperitoneally on days 3 and 5. On day 7, the right buccal pouch mucosa was superficially irritated with a calibrated 18 gauge needle. In untreated animals, severe ulcerative mucositis was induced in at least 80% of the animals by day 10.

[0114] For each administration of the vehicle control (placebo) or morphogen, administration was performed by first gently drying the cheek pouch mucosa, then providing an even application over the mucosal surface of the vehicle or morphogen material. A hydroxypropylcellulose-based coating was used to maintain contact of the morphogen with the mucosa. This coating provided at least 4 hours of contact time.

[0115] On day 12, two animals in each group were sacrificed for histological studies. The right buccal pouch mucosa and underlying connective tissue were dissected and fixed in 10% formalin using standard dissection and histology procedures. The specimens were mounted in paraffin and prepared for histologic examination. Sections then were stained with hematoxylin and eosin and were examined blindly by three oral pathologists with expertise in hamster histology and scored blind against a standard mucositis panel. The extent of atrophy, cellular infiltration, connective tissue breakdown, degree of ulceration and epithelialization were assessed.

[0116] The mean mucositis score for each group was determined daily for each experimental group for a period of 21 days by photography and visual examination of the right buccal cheek pouch. Differences between groups were determined using a standard 't' test, e.g., the Students' 't' test. In addition, data was evaluated between groups by comparing the numbers of animals with severe mucositis using Chi Square statistical analysis. The significance of differences in mean daily weights also was determined.

[0117] The experimental results are presented in Fig. 5, which graphs the effect of morphogen (high dose, squares; low dose, diamonds) and placebo (circles) on mean mucositis scores. Both low and high morphogen doses inhibit lesion formation significantly in a dose-dependent manner. In addition, histology results consistently showed significantly reduced amounts of tissue atrophy, cellular debris, and immune effector cells, including macrophages and activated neutrophils, in the morphogen-treated animals, as compared with the untreated, control animals.

Example 9. Morphogen Effect on Fibrogenesis and Scar Tissue Formation

[0118] The morphogens described herein induce tissue morphogenesis of damaged or lost tissue. The ability of these proteins to regenerate new tissue enhances the anti-inflammatory effect of these proteins. Provided below are a series of in vitro experiments demonstrating the ability of morphogens to induce migration and accumulation of mesenchymal cells. In addition, the experiments demonstrate that morphogens, unlike TGF- β , do not stimulate fibrogenesis or scar tissue formation. Specifically, morphogens do not stimulate production of collagen, hyaluronic acid (HA) or metalloproteinases in primary fibroblasts, all of which are required for fibrogenesis or scar tissue formation. By contrast, TGF- β , a known inducer of fibrosis, but not of tissue morphogenesis, does stimulate production of these fibrosis markers.

[0119] Chemotaxis and migration of mesenchymal progenitor cells were measured in modified Boyden chambers essentially as described by Fava, R.A. et al (1991) *J. Exp. Med.* 173: 1121-1132, using polycarbonate filters of 2, 3 and 8 micron ports to measure migration of progenitor neutrophils, monocytes and fibroblasts. Chemotaxis was measured over a range of morphogen concentrations, e.g., 10^{-20} M to 10^{-12} M OP-1. For progenitor neutrophils and monocytes, 10^{-18} - 10^{-17} M OP-1 consistently induced maximal migration, and 10^{-14} to 10^{-13} M OP-1 maximally induced migration of progenitor fibroblasts. In all cases the chemotactic activity could be inhibited with anti-OP-1 antibody. Similar migration activities also were measured and observed with TGF- β .

[0120] The effect of morphogen on fibrogenesis was determined by evaluating fibroblast production of hyaluronic acid (HA), collagen, collagenase and tissue inhibitor of metalloproteinases (TIMP).

[0121] Human fibroblasts were established from explants of infant foreskins and maintained in monolayer culture using standard culturing procedures. (See, for example, (1976) *J. Exp. Med.* 144:1188-1203.) Briefly, fibroblasts were grown in maintenance medium consisting of Eagle's MEM, supplemented with nonessential amino acids, ascorbic acid (50 µg/ml), NaHCO₃ and HEPES buffers (pH 7.2), penicillin (100 U/ml), streptomycin (100 µg/ml), amphotericin B (1 µg/ml) and 9% heat inactivated FCS. Fibroblasts used as target cells to measure chemotaxis were maintained in 150 mm diameter glass petri dishes. Fibroblasts used in assays to measure synthesis of collagen, hyaluronic acid, collagenase and tissue inhibitors of metalloproteinases (TIMP) were grown in 100 mm diameter plastic tissue culture petri dishes.

[0122] The effects of morphogen on fibroblast production of hyaluronic acid, collagens, collagenase and TIMP were determined by standard assays (See, for example, Posttethwaite et al. (1989) *J. Clin. Invest.* 83: 629-636, Posttethwaite (1988) *J./Cell Biol.* 106:311-318 and Clark et al (1985) *Arch. Bio-chem Biophys.* 241:36-44). For these assays, fibroblasts were transferred to 24-well tissue culture plates at a density of 8×10^4 cells per well. Fibroblasts were grown

confluence in maintenance medium containing 9% FCS for 72 h and then grown in serum-free maintenance medium for 24 h. Medium was then removed from each well and various concentrations of OP-1 (recombinantly produced mature or soluble form) or TGF- β -1 (R&D Systems, Minneapolis) in 50 μ l PBS were added to triplicate wells containing the confluent fibroblast monolayers. For experiments that measured production of collagenase and TIMP, maintenance medium (450 μ l) containing 5% FCS was added to each well, and culture supernatants were harvested from each well 48 h later and stored at -70°C until assayed. For experiments that assessed HA production, maintenance medium (450 μ l) containing 2.5% FCS was added to each well, and cultures grown for 48 h. For experiments that measured fibroblast production of collagens, serum-free maintenance medium (450 μ l) without non-essential amino acids was added to each well and cultures grown for 72 h. Fibroblast production of HA was measured by labeling newly synthesized glycosaminoglycans (GAG) with [3 H]-acetate the last 24 h of culture and quantitating released radioactivity after incubation with hyaluronidase from *Streptomyces hyalurolyticus* (ICN Biochemicals, Cleveland, OH) which specifically degrades hyaluronic acid. Production of total collagen by fibroblasts was measured using a collagenase-sensitive protein assay that reflects [3 H]-proline incorporation the last 24 h of culture into newly synthesized collagens. Collagenase and TIMP protein levels in fibroblast cultures supernatants was measured by specific ELISAs.

[0123] As shown in Fig. 6, OP1 does not stimulate significant collagen or HA production, as compared with TGF- β . In the figure, panel A shows OP-1 effect on collagen production, panel B shows TGF- β effect on collagen production, and panels C and D show OP-1 (panel C) and TGF- β (panel D) effect on HA production. The morphogen results were the same whether the soluble or mature form of OP1 was used. By contrast, the latent form of TGF- β (e.g., pro domain-associated form of TGF- β) was not active.

Example 10. Morphogen Inhibition of Epithelial Cell Proliferation

[0124] This example demonstrates the ability of morphogens to inhibit epithelial cell proliferation *in vitro*, as determined by 3 H-thymidine uptake using culture cells from a mink lung epithelial cell line (ATCC No. CCL 64), and standard mammalian cell culturing procedures. Briefly, cells were grown to confluence in Eagle's minimum essential medium (EMEM) supplemented with 10% fetal bovine serum (FBS), 200 units/ml penicillin, and 200 μ g/ml streptomycin, and used to seed a 48-well cell culture plate at a cell density of 200,000 cells per well. When this culture became confluent, the media was replaced with 0.5 ml of EMEM containing 1% FBS and penicillin/streptomycin and the culture incubated for 24 hours at 37°C. Morphogen test samples in EMEM containing 5% FBS then were added to the wells, and the cells incubated for another 18 hours. After incubation, 1.0 μ Ci of 3 H-thymidine in 10 μ l was added to each well, and the cells incubated for four hours at 37°C. The media then was removed and the cells washed once with ice-cold phosphate-buffer saline and DNA precipitated by adding 0.5 ml of 10% TCA to each well and incubating at room temperature of 15 minutes. The cells then were washed three times with ice-cold distilled water, lysed with 0.5 ml 0.4 M NaOH, and the lysate from each well then transferred to a scintillation vial and the radioactivity recorded using a scintillation counter (Smith-Kline Beckman).

[0125] The results are presented in Table III, below. The anti-proliferative effect of the various morphogens tested was expressed as the counts of 3 H-thymidine (\times 1000) integrated into DNA, and were compared with untreated cells (negative control) and TGF- β (1 ng), a local-acting factor also known to inhibit epithelial cell proliferation. COP-5 and COP-7 are biosynthetic constructs that previously have been shown to have osteogenic activity, capable of inducing the complete cascade resulting in endochondral bone formation in a standard rat bone assay (see U.S. Pat. No. 5,011,691.) The morphogens significantly inhibit epithelial cell proliferation. Similar experiments, performed with the morphogens COP-16, bOP (bone-purified osteogenic protein, a dimeric protein comprising CBMP2 and OP-1), and recombinant OP-1, also inhibit cell proliferation. bOP and COP-16 also induce endochondral bone formation (see US Pat. No. 4,968,590 and 5,011,691.)

TABLE III

	Thymidine uptake (\times 1000)
control	50.048, 53.692
COP-7-1 (10 ng)	11.874
COP-7-2 (3 ng)	11.136
COP-5-1 (66 ng)	16.094
COP-5-2 (164 ng)	14.43
TGF- β (1 ng)	1.86, 1.478

Example 11. Morphogen Treatment of a Systemic Inflammatory Disease

[0126] The following example provides a rat adjuvant-induced arthritis model for demonstrating morphogen efficacy in treating arthritis and other systemic inflammatory diseases. Rat adjuvant-induced arthritis induces a systemic inflammatory disease with bone and cartilage changes similar to those observed in rheumatoid arthritis, but in an accelerated time span (see, for example, Pearson (1964) *Arth. Rheum.* 7:80). A detailed description of the protocol is provided in Walz, et al., (1971) *J. Pharmac. Exp. Ther.* 178:223-231.

[0127] Briefly, Sprague-Dawley female rats (e.g., Charles River Laboratories, Wilmington, MA) are randomized into 3 groups: control; morphogen, low dose (e.g., 1-10 µg/kg weight per day) and morphogen, high dose (e.g., 10-20 µg/kg weight per day), referred to as Groups 1, 2, and 3, respectively.

[0128] Adjuvant arthritis is induced in all three groups by injection of 0.05 ml of a suspension of 1.5% dead *Mycobacterium butyricum* in mineral oil into the subplantar surface of the right hind paw. On Day 18 after adjuvant injection, the limb volumes of both hind limb are determined. In the absence of morphogen treatment, a systemic arthritic condition is induced in adjuvant-injected rats by this time, as determined by significant swelling of the uninjected hind limbs (<2.3 ml, volume measured by mercury displacement). Subsequent determinations of paw edema and x-ray scores are made on the uninjected hind limb. Rats in Group 2 and 3 also are dosed orally daily, beginning on Day 1, with morphogen. Limb volumes are recorded on Days 29 and 50 after adjuvant injection and edema determined by volume difference compared to Day 18. The uninjected hind limb on each rat is x-rayed on Day 50 and the joint damage assayed on an arbitrary scale of 1 to 10 (1=no damage, 10=maximum damage). Data on differences between control and treated groups (Day 29 edema, Day 50 edema and Day 50 x-ray scores) are analyzed by using a standard "t-test. Morphogen-treated rats show consistently reduced joint damage (e.g., decreased in edema and in x-ray scores) as compared with untreated control rats.

[0129] As another, alternative example, Groups 2 and 3 are dosed daily with morphogen beginning on Day 18 and continuing through Day 50 to demonstrate the efficacy of morphogens in arthritic animals.

Example 12. Morphogen Inhibition of Localized Edema

[0130] The following example demonstrates morphogen efficacy in inhibiting a localized inflammatory response in a standard rat edema model. Experimental rats (e.g., Long-Evans from Charles River Laboratories, Wilmington, MA) are divided into three groups: Group 1, a negative control, which receives vehicle alone; Group 2, a positive control, to which is administered a well-known characterized anti-inflammatory agent (e.g., indomethacin), and Group 3, to which morphogen is provided.

[0131] Groups 2 and 3 may be further subdivided to test low, medium and high doses (e.g., Group 2: 1.0 mg/kg, 3.0 mg/kg and 9.0 mg/kg indomethacin; Group 3: 0.1-5µg; 5-20µg, and 20-50µg of morphogen). Sixty minutes after indomethacin or morphogen is provided to the rats of Group 2 or 3 (e.g., as by injection into the tail vein, or by oral gavage) inflammation is induced in all rats by a sub-plantar injection of a 1% carrageenin solution (50µl) into the right hind paw. Three hours after carrageenin administration paw thickness is measured as an indication of edema (e.g., swelling) and induced inflammatory response to the injected carrageenin solution.

[0132] Significant swelling is evident in untreated rats by three hours after carrageenin injection. Inflammation also is measured by histology by standard means, following euthanasia e.g.: the right hind paw from each animal is removed at the ankle joint and weighed and foot pad tissue is fixed in 10% neutral buffered formalin, and slides prepared for visual examination by staining the prepared tissue with hematoxylin and eosin.

[0133] The morphogen-treated rats show substantially reduced edema induction following carrageenin injection as compared with the untreated rats.

Example 13. Morphogen Treatment of Allergic Encephalomyelitis

[0134] The following example demonstrates morphogen efficacy in treating experimental allergic encephalomyelitis (EAE) in a rat. EAE is a well-characterized animal model for multiple sclerosis, an autoimmune disease. A detailed description of the protocol is disclosed in Kuruvilla, et al., (1991) *PNAS* 88:2918-2921.

[0135] Briefly, EAE is induced in rats (e.g., Long-Evans, Charles River Laboratories, Wilmington, MA) by injection of a CNS tissue (e.g., spinal cord) homogenate in complete Freund's adjuvant (CFA) on days -44, -30 and 0 (last day of immunization), by subcutaneous injection to three sites on the animal's back. Morphogen is administered daily by interperitoneal injection beginning on day -31. Preferably, a series of morphogen dose ranges is evaluated (e.g., low, medium and high) as for Example 12, above.) Control rats receive morphogen vehicle only (e.g. 0.9% NaCl or buffered saline). Rats are examined daily for signs of disease and graded on an increasing severity scale of 0-4.

[0136] In the absence of morphogen treatment, significant neurological dysfunction (e.g., hind and fore limb weakness, progressing to total hind limb paralysis) is evident by day +7 to +10. Hematology, serum chemistry profiles and

histology are performed to evaluate the degree of tissue necropsy using standard procedures. Morphogen treatment significantly inhibits the neurological dysfunction normally evident in an EAE animal. In addition, the histopathological markers typically associated with EAE are absent in the morphogen-treated animals

5 Example 14. Morphogen Treatment of Collagen-Induced Arthritis

[0137] The following example demonstrates the efficacy of morphogens in inhibiting the inflammatory response in a collagen-induced arthritis (CIA) in a rat. CIA is a well-characterized animal model for rheumatoid arthritis, an autoimmune disease. The protocol disclosed is essentially that disclosed in Kuruvilla et al., (1991) PNAS 88:2918-2921. 10 Briefly, CIA is induced in experimental rats (e.g., Long-Evans, Charles River Laboratories, Wilmington), by multiple intradermal injection of bovine Type II collagen (e.g., 100 μ g) in CFA (0.2 ml) on Day 1. Animals are divided into two groups: Group 1, control animals, which receive vehicle alone, and Group 2: morphogen-treated animals, which, preferably, are subdivided into low, medium and high dose ranges, as described for Example 13, above. Morphogen is administered daily (e.g., by tail vein injection) beginning at different times following collagen injection, e.g., beginning 15 on day 7, 14, 28, 35 and 42. Animals are evaluated visually and paw thickness and body weight is monitored throughout the experiment. Animals are sacrificed on day 60 and the proximal and distal limb joints, and ear, tail and spinal cord prepared for histological evaluation as described for Examples 12 and 13, above. In a variation of the experiment, morphogen may be administered for prescribed periods, e.g., five day periods, beginning at different times following collagen injection (e.g., on days 0-4, 7-11, 14-18, 28-32.)

[0138] In the absence of morphogen treatment, an arthritic condition typically is induced by 30 days post collagen injection. In morphogen-treated animals, CIA is suppressed and the histopathological changes typically evidenced in control CIA-induced animals are absent: e.g., accumulations of activated mononuclear inflammatory cells and fibrous connective tissue. In addition, consistent with the results in Example 7, above, serum anti-collagen antibody titers are suppressed significantly in the morphogen-treated animals.

25 Example 15. Screening Assay for Candidate Compounds which Alter Endogenous Morphogen Levels

[0139] Candidate compound(s) which may be administered to affect the level of a given morphogen may be found using the following screening assay, in which the level of morphogen production by a cell type which produces measurable levels of the morphogen is determined with and without incubating the cell in culture with the compound, in order to assess the effects of the compound on the cell. This can be accomplished by detection of the morphogen either at the protein or RNA level. A more detailed description also may be found in USSN 752,861.

15.1 Growth of Cells in Culture

[0140] Cell cultures of kidney, adrenals, urinary bladder, brain, or other organs, may be prepared as described widely in the literature. For example, kidneys may be explanted from neonatal or new born or young or adult rodents (mouse or rat) and used in organ culture as whole or sliced (1-4 mm) tissues. Primary tissue cultures and established cell lines, also derived from kidney, adrenals, urinary, bladder, brain, mammary, or other tissues may be established in multiwell plates (6 well or 24 well) according to conventional cell culture techniques, and are cultured in the absence or presence of serum for a period of time (1-7 days). Cells may be cultured, for example, in Dulbecco's Modified Eagle medium (Gibco, Long Island, NY) containing serum (e.g., fetal calf serum at 1%-10%, Gibco) or in serum-deprived medium, as desired, or in defined medium (e.g., containing insulin, transferrin, glucose, albumin, or other growth factors).

[0141] Samples for testing the level of morphogen production includes culture supernatants or cell lysates, collected periodically and evaluated for OP-1 production by immunoblot analysis (Sambrook et al., eds., 1989, Molecular Cloning, Cold Spring Harbor Press, Cold Spring Harbor, NY), or a portion of the cell culture itself, collected periodically and used to prepare polyA+ RNA for RNA analysis. To monitor *de novo* OP-1 synthesis, some cultures are labeled according to conventional procedures with an 35 S-methionine/ 35 S-cysteine mixture for 6-24 hours and then evaluated to OP-1 synthesis by conventional immunoprecipitation methods.

50 15.2 Determination of Level of Morphogenic Protein

[0142] In order to quantitate the production of a morphogenic protein by a cell type, an immunoassay may be performed to detect the morphogen using a polyclonal or monoclonal antibody specific for that protein. For example, OP-1 may be detected using a polyclonal antibody specific for OP-1 in an ELISA, as follows.

[0143] 1 μ g/100 μ l of affinity-purified polyclonal rabbit IgG specific for OP-1 is added to each well of a 96-well plate and incubated at 37°C for an hour. The wells are washed four times with 0.167M sodium borate buffer with 0.15 M NaCl (BSB), pH 8.2, containing 0.1% Tween 20™. To minimize non-specific binding, the wells are blocked by filling

completely with 1% bovine serum albumin (BSA) in BSB and incubating for 1 hour at 37°C. The wells are then washed four times with BSB containing 0.1% Tween 20. A 100 µl aliquot of an appropriate dilution of each of the test samples of cell culture supernatant is added to each well in triplicate and incubated at 37°C for 30 min. After incubation, 100 µl biotinylated rabbit anti-OP-1 serum (stock solution is about 1 mg/ml and diluted 1:400 in BSB containing 1% BSA before use) is added to each well and incubated at 37°C for 30 min. The wells are then washed four times with BSB containing 0.1% Tween 20. 100 µl strepavidin-alkaline (Southern Biotechnology Associates, Inc. Birmingham, Alabama, diluted 1:2000 in BSB containing 0.1% Tween 20 before use) is added to each well and incubated at 37°C for 30 min. The plates are washed four times with 0.5M Tris buffered Saline (TBS), pH 7.2. 50µl substrate (ELISA Amplification System Kit, Life Technologies, Inc., Bethesda, MD) is added to each well incubated at room temperature for 15 min. Then, 50 µl amplifier (from the same amplification system kit) is added and incubated for another 15 min at room temperature. The reaction is stopped by the addition of 50 µl 0.3 M sulphuric acid. The OD at 490 nm of the solution in each well is recorded. To quantitate OP-1 in culture media, a OP-1 standard curve is performed in parallel with the test samples.

[0144] Polyclonal antibody may be prepared as follows. Each rabbit is given a primary immunization of 100 ug/500 µl E. coli produced OP-1 monomer (amino acids 328-431 in SEQ ID NO:5) in 0.1% SDS mixed with 500 µl Complete Freund's Adjuvant. The antigen is injected subcutaneously at multiple sites on the back and flanks of the animal. The rabbit is boosted after a month in the same manner using incomplete Freund's Adjuvant. Test bleeds are taken from the ear vein seven days later. Two additional boosts and test bleeds are performed at monthly intervals until antibody against OP-1 is detected in the serum using an ELISA assay. Then, the rabbit is boosted monthly with 100 µg of antigen and bled (15 ml per bleed) at days seven and ten after boosting.

[0145] Monoclonal antibody specific for a given morphogen may be prepared as follows. A mouse is given two injections of E. coli produced OP-1 monomer. The first injection contains 100µg of OP-1 in complete Freund's adjuvant and is given subcutaneously. The second injection contains 50 µg of OP-1 in incomplete adjuvant and is given intraperitoneally. The mouse then receives a total of 230 µg of OP-1 (amino acids 307-431 in SEQ ID NO:5) in four intraperitoneal injections at various times over an eight month period. One week prior to fusion, both mice are boosted intraperitoneally with 100 µg of OP-1 (307-431) and 30 µg of the N-terminal peptide (Ser₂₉₃-Asn₃₀₉-Cys) conjugated through the added cysteine to bovine serum albumin with SMCC crosslinking agent. This boost was repeated five days (IP), four days (IP), three days (IP) and one day (IV) prior to fusion. The mouse spleen cells are then fused to myeloma (e.g., 653) cells at a ratio of 1:1 using PEG 1500 (Boeringer Mannheim), and the cell fusion is plated and screened for OP-1-specific antibodies using OP-1 (307-431) as antigen. The cell fusion and monoclonal screening then are according to standard procedures well described in standard texts widely available in the art.

[0146] The invention may be embodied in other specific forms and the present embodiments are therefore to be considered in all respects as illustrative and not restrictive, the scope of the invention being indicated by the appended claims.

35 SEQUENCE LISTING

[0147]

40 (1) GENERAL INFORMATION:

(i) APPLICANT:

KUBERASAMPATH, THANGAVEL
 45 PANG, ROY H.L.
 OPPERMANN, HERMANN
 RUEGER, DAVID C.
 COHEN, CHARLES M.
 OZKAYNAK, ENGIN
 SMART, JOHN

(ii) TITLE OF INVENTION: MORPHOGEN-INDUCED MODULATION OF INFLAMMATORY RESPONSE

(iii) NUMBER OF SEQUENCES: 33

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CREATIVE BIOMOLECULES

(B) STREET: 35 SOUTH STREET
(C) CITY: HOPKINTON
(D) STATE: MASSACHUSETTS
(E) COUNTRY: U.S.A.
5 (F) ZIP:

(v) COMPUTER READABLE FORM:

10 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent In Release #1.0, Version #1.25

15 (vii) PRIOR APPLICATION DATA:

15 (A) APPLICATION NUMBER: US 667,274
(B) FILING DATE: 11-MAR-1991

20 (vii) PRIOR APPLICATION DATA:

20 (A) APPLICATION NUMBER: US 753,059
(B) FILING DATE: 30-AUG-1991

25 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: US 752,764
(B) FILING DATE: 30-AUG-1991

30 (2) INFORMATION FOR SEQ ID NO:1:

30 (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 97 amino acids
(B) TYPE: amino acids
(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

40 (A) NAME: Generic Sequence 1

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50

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	Xaa							
	1							5
5	Xaa							
					10			15
	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa
					20		25	Xaa
10	Cys	Xaa						
					30		35	Xaa
	Xaa							
					40		45	50
15	Xaa							
					55		60	Cys
	Cys	Xaa						
					65		70	Xaa
	Xaa							
					75		80	Xaa
	Xaa							
					85		90	Cys
	Xaa	Cys	Xaa					
		95						

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME: Generic Sequence 2
(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa
 1 5
 Xaa
 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 20 25
 Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
 30 35
 Xaa
 40 45 50

Xaa Cys
 55 60
 Cys Xaa
 65 70
 Xaa
 75 80
 Xaa Cys
 85 90
 Xaa Cys Xaa
 95

(2) INFORMATION FOR SEQ ID NO:3:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: Generic Sequence 3

25 (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Tyr Val Xaa Phe
 1 5
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 10
 Xaa Ala Pro Gly Xaa Xaa Xaa Ala
 15 20
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 25 30
 Xaa Pro Xaa Xaa Xaa Xaa Xaa
 35
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 40 45
 Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
 50
 Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55 60
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 65
 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70 75
 Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 80
 Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 85 90
 Xaa Cys Gly Cys Xaa
 95

55

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

5
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

10
 (A) NAME: Generic Sequence 4

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

15

Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
1						5				10
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa		
						15				
Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Xaa			
	20				25					
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa			
			30			35				
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa				
					40					
Asn	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa			
			45			50				
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa			
					55					
Xaa	Cys									
			60			65				
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa			
				70						
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa				
			75			80				
Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa			
				85						
Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa			
			90			95				
Xaa	Cys	Gly	Cys	Xaa						
				100						

(2) INFORMATION FOR SEQ ID NO:5:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(ix) FEATURE:

55
 (A) NAME: hOP-1 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln
5	1				5				
	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
	10					15			
	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala
		20					25		
	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
10		30					35		
	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45	
	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
					50				
15	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
		65					70		
	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
20		75					80		
	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90	
	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
					95				
25	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
	100					105			
	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
		110					115		
	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120						125	
30	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130						135
	Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:6:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein
(ix) FEATURE:

- (A) NAME: mOP-1 (mature form)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

50	Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln
	1				5				
	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
	10					15			
	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala
55		20					25		
	Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
			30					35	

	Ala	Cys	Lys	Lys 40	His	Glu	Leu	Tyr	Val
5	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp 45
	Trp	Ile	Ile	Ala	Pro	Glu 50	Gly	Tyr	Ala
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu 70	Cys	Ala
10		65							
	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn 80	Ala
			75						
	Thr	Asn	His	Ala 85	Ile	Val	Gln	Thr	Leu 90
15									
	Val	His	Phe	Ile	Asn 95	Pro	Asp	Thr	Val
	Pro	Lys	Pro	Cys	Cys	Ala 105	Pro	Thr	Gln
20	100								
	Leu	Asn	Ala	Ile	Ser	Val	Leu 115	Tyr	Phe
	110								
	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu 125	Lys
25			120						
	Lys	Tyr	Arg	Asn 130	Met	Val	Val	Arg	Ala 135
	Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (ix) FEATURE:

(A) NAME: hOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
5	1				5				
	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
	10					15			
	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
	20						25		
	Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
10		30						35	
	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
				40					45
	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
15					50				
	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
	55					60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
	65						70		
	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
20		75							

25	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85						90
	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
					95				
	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
30	100					105			
	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		110					115		
	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
35		120						125	
	Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130						135
	Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:8:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein
(ix) FEATURE:

50 (A) NAME: mOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

	Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
5	1				5				
	Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
	10					15			
	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
		20					25		
	Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
10			30					35	
	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45	
	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
					50				
15	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
		55				60			
	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
		65					70		
	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
20			75					80	
	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90	
	Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
					95				
25	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
		100				105			
	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
		110					115		
	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
			120					125	

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Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:9:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:

- (A) NAME: CBMP-2A(fx)

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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5 Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser
 1 5 10
 Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
 15 20
 Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu
 25 30
 Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser
 35 40
 Thr Asn His Ala Ile Val Gln Thr Leu Val Asn
 45 50 55
 Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
 60 65
 Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 70 75
 Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys
 80 85
 Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
 90 95
 20 Cys Arg
 100

(2) INFORMATION FOR SEQ ID NO:10:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:

35 (A) NAME: CBMP-2B(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

40 Cys Arg Arg His Ser
 1 5
 Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn
 10 15
 Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala
 20 25

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Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu
 30 35
 Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
 40 45
 Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser
 50 55 60
 Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu
 65 70
 Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Tyr
 75 80
 Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 85 90
 Val Val Glu Gly Cys Gly Cys Arg
 95 100

(2) INFORMATION FOR SEQ ID NO:11:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:

- (A) NAME: DPP(fx)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser
 1 5 10
 Asp Val Gly Trp Asp Asp Trp Ile Val Ala Pro
 15 20
 Leu Gly Tyr Asp Ala Tyr Tyr Cys His Gly Lys
 25 30
 Cys Pro Phe Pro Leu Ala Asp His Phe Asn Ser
 35 40
 Thr Asn His Ala Val Val Gln Thr Leu Val Asn
 45 50 55
 Asn Asn Asn Pro Gly Lys Val Pro Lys Ala Cys
 60 65
 Cys Val Pro Thr Gln Leu Asp Ser Val Ala Met
 70 75
 Leu Tyr Leu Asn Asp Gln Ser Thr Val Val Leu
 80 85
 Lys Asn Tyr Gln Glu Met Thr Val Val Gly Cys
 90 95
 Gly Cys Arg
 100

55 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:

(A) NAME: Vgl(fx)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	Cys	Lys	Lys	Arg	His	Leu	Tyr	Val	Glu	Phe	Lys
	1					5					10
15	Asp	Val	Gly	Trp	Gln	Asn	Trp	Val	Ile	Ala	Pro
				15					20		
	Gln	Gly	Tyr	Met	Ala	Asn	Tyr	Cys	Tyr	Gly	Glu
				25				30			
20	Cys	Pro	Tyr	Pro	Leu	Thr	Glu	Ile	Leu	Asn	Gly
				35			40				
	Ser	Asn	His	Ala	Ile	Leu	Gln	Thr	Leu	Val	His
				45			50			55	
25	Ser	Ile	Glu	Pro	Glu	Asp	Ile	Pro	Leu	Pro	Cys
					60				65		
	Cys	Val	Pro	Thr	Lys	Met	Ser	Pro	Ile	Ser	Met
					70				75		
30	Leu	Phe	Tyr	Asp	Asn	Asn	Asp	Asn	Val	Val	Leu
				80			85				
	Arg	His	Tyr	Glu	Asn	Met	Ala	Val	Asp	Glu	Cys
				90				95			
	Gly	Cys	Arg								
			100								

35 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein
 (ix) FEATURE:

45 (A) NAME: Vgr-1(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

50

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5 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln
 1 5 10
 Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro
 15 20
 Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu
 25 30
 Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
 35 40
 Thr Asn His Ala Ile Val Gln Thr Leu Val His
 45 50 55
 Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys
 60 65
 Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val
 70 75

20 Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu
 80 85
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys
 90 95
 Gly Cys His
 25 100

(2) INFORMATION FOR SEQ ID NO:14:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- 35 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (F) TISSUE TYPE: BRAIN

45 (ix) FEATURE:

- 45 (D) OTHER INFORMATION: /product= "GDF-1 (fx)"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

40 Cys Xaa Xaa Xaa Xaa
|
5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS
(F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (D) OTHER INFORMATION:/standard_name= "hOP1"

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	GGTGCGGGCC CGGAGCCCCG AGCCCCGGTA GCGCGTAGAG CCCGGCGCG ATG CAC GTG	57
10	Met His Val	
	1	
	CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
	Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
	5 10 15	
15	CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
	Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
	20 25 30 35	
20	GAG CTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
	Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
	40 45 50	
25		
30		
35		
40		
45		
50		
55		

	CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg 55 60 65	249
5	CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met 70 75 80	297
10	CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GGC GGC GGG CCC GGC Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Pro Gly 85 90 95	345
15	GGC CAG CGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly 100 105 110 115	393
20	CCC CCT CTG GCC AGC CTG CAA GAT ACC CAT TTC CTC ACC GAC GCC GAC Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp 120 125 130	441
25	ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe 135 140 145	489
30	CAC CCA CGC TAC CAC CAT CGA GAG TTC CCG TTT GAT CTT TCC AAG ATC His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile 150 155 160	537
35	CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CCG ATC TAC AAG GAC Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp 165 170 175	585
40	TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CCG ATC AGC GTT TAT Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr 180 185 190 195	633
45	CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu 200 205 210	681
50	GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp 215 220 225	729
	ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu 230 235 240	777
	GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro 245 250 255	825

	AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro 260 265 270 275	873
5	TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CCC AGC ATC Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290	921
10	CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305	969
15	AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320	1017
20	AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1065
25	CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1113
30	GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
35	AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1209
40	CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1257
45	ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305
50	TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His 420 425 430	1351
	GAGAATTCAAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
	GAACCAGCAG ACCAACTGCC TTTTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
	TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTT CAGTGGCAGC	1531
	ATCCAATGAA CAAGATCTA CAAGCTGTGC AGGCCAAAACC TAGCAGGAAA AAAAAACAAAC	1591

5	GCATAAAGAA AAATGGCCGG GCCAGGTCA TGGCTGGGAA GTCTCAGCCA TGACCGACT	1651
	CGTTTCCAGA GGTAAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
	GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGGCAAAG GAAAATTGAC CGGGAAGTTC	1771
	CTGTAATAAA TGTACAATA AACGAATGA ATGAAAAAAA AAAAAAAAAA A	1822

10 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 431 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

20 (D) OTHER INFORMATION: /Product="OP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID No:17:

25	Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala	
	1 5 10 15	
30	Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser	
	20 25 30	
35	Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser	
	35 40 45	
40	Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu	
	50 55 60	
45	Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro	
	65 70 75 80	
50	Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly	
	85 90 95	
	Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser	
	100 105 110	
	Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr	
	115 120 125	
	Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys	
	130 135 140	
	Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu	
	145 150 155 160	

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
 165 170 175
 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
 180 185 190
 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
 195 200 205
 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:18:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1873 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MURIDAE

(F) TISSUE TYPE: EMBRYO

10 (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1393

(D) OTHER INFORMATION: /note= "MOP1 (cDNA)"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

20	CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCCTCCGCTG CCACCTGGGG	60
	CGGCGCGGGC CGGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC Met His Val Arg	115
	1	
25	TCG CTG CGC GCT GCG GCG CCA CAC ACC TTC GTG GCG CTC TGG GCG CCT Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro	163
	5 10 15 20	
30	CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu	211
	25 30 35	
35	G TG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg	259
	40 45 50	
40	GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CGC Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro	307
	55 60 65	
45	CGC CCG CAC CTC CAG CGA AAG CAT AAT TCG GCG CCC ATG TTC ATC TTG Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu	355
	70 75 80	
50	GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC CGA CAG Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln	403
	85 90 95 100	

	GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG CCC CCT Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro 105 110 115	451
5	TTA GCC AGC CTG CAG GAC AGC CAT TTC CTC ACT GAC GCC GAC ATG GTC Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val 120 125 130	499
10	ATG AGC TTC GTC AAC CTA GTG GAA CAT GAC AAA GAA TTC TTC CAC CCT Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro 135 140 145	547
15	CGA TAC CAC CAT CGG GAG TTC CGG TTT GAT CTT TCC AAG ATC CCC GAG Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu 150 155 160	595
	GGC GAA CGG GTG ACC GCA GCC GAA TTC ACC ATC TAT AAG GAC TAC ATC Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile 165 170 175 180	643
20	CGG GAG CGA TTT GAC AAC GAG ACC TTC CAG ATC ACA GTC TAT CAG GTG Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr Val Tyr Gln Val 185 190 195	691
25	CTC CAG GAG CAC TCA GGC AGG GAG TCG GAC CTC TTC TTG CTG GAC AGC Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe Leu Asp Ser 200 205 210	739
30	CGC ACC ATC TGG GCT TCT GAG GAG GGC TGG TTG GTG TTT GAT ATC ACA Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr 215 220 225	787
	GCC ACC AGC AAC CAC TGG GTG GTC AAC CCT CGG CAC AAC CTG GGC TTA Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu 230 235 240	835
35	CAG CTC TCT GTG GAG ACC CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu 245 250 255 260	883
40	GCA GGC CTG ATT GGA CGG CAT GGA CCC CAG AAC AAG CAA CCC TTC ATG Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met 265 270 275	931
45	GTG GCC TTC TTC AAG GCC ACG GAA GTC CAT CTC CGT AGT ATC CGG TCC Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg Ser Ile Arg Ser 280 285 290	979
	ACG GGG GGC AAG CAG CGC AGC CAG AAT CGC TCC AAG ACG CCA AAG AAC Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn 295 300 305	1027
50		

	CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp 310 315 320	1075
5	CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp 325 330 335 340	1123
10	CTT GGC TGG CAG GAC TCG ATC ATT GCA CCT GAA GCC TAT GCT GCC TAC Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr 345 350 355	1171
15	TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala 360 365 370	1219
20	ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp 375 380 385	1267
25	ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser 390 395 400	1315
30	GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Tyr Arg 405 410 415 420	1363
35	AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCCTG Asn Met Val Val Arg Ala Cys Gly Cys His 425 430	1413
40	ACCTTTGCCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCTGAGCC TTCCCTCACCC TCCCAACCGG AAGCATGTAA GGGTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT GGCACGTGAC GGACAAGATC CTACCAAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCCCTGGC GCTCTGAGTC TTGAGGGAGT AATCGCAAGC CTCGTTCAAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCGCTGGCG TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT 45 GAATGAAAAA AAAAAAAA AAAAAAAA AAAAGAATTG	1473 1533 1593 1653 1713 1773 1833 1873

50 (2) INFORMATION FOR SEQ ID N0:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: /product= "mOP1-PP"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

10

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1 5 10 15

15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
 20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
 35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
 50 55 60

20

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
 85 90 95

25

Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
 100 105 110

30

Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
 115 120 125

Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
 130 135 140

35

Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
 145 150 155 160

40

Lys Ile Pro Glu Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr
 165 170 175

Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
 180 185 190

Val Tyr Gln Val Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
 195 200 205

45

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5	Leu	Leu	Asp	Ser	Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val
	210						215				220					
10	Phe	Asp	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His
	225						230				235			240		
15	Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile
						245			250				255			
20	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys
						260			265			270				
25	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg
						275			280			285				
30	Ser	Ile	Arg	Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys
						290			295			300				
35	Thr	Pro	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala	Glu	Asn
						305			310			315			320	
40	Ser	Ser	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
						325			330			335				
45	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly
						340			345			350				
50	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser
						355			360			365				
55	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe
						370			375			380				
60	Ile	Asn	Pro	Asp	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu
						385			390			395			400	
65	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu
						405			410			415				
70	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His		
						420			425			430				

(2) INFORMATION FOR SEQ ID NO:20:

45

- (A) LENGTH: 1723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(v) REC'D BY E. W. FISHER

(A) ORGANISM: *Homo sapiens*
(F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 490..1696
 5 (D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

10	GGCGCCGGCA GACCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA	60
	GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCAGG AGGCCTGGGA GCAACAGCTC	120
	CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCATC GCCCCCTGCGC TGCTCGGACC	180
15	GCGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT	240
	CCGCAGACTA GCCCCGGCCT CGAGGGGGTG GCGTCCCCGT CCTCTCCGTG CAGGAGCCAG	300
20	GACAGGTGTC GCGCGGGGGG GCTCCAGGGA CGCCGCCTGA GGCCGGCTGC CGCCCGTCC	360
	CGCCCCCCCC CGCGGGGGGG CGCCCGCCGA GCCCAGCCTC TTGCGCGTGC GGGCGTCCCC	420
	AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC	480
25	CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG	528
	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu	
	1 5 10	
30	GCG CTA TGC GCG CTG GGC GGG GGC CCC GGC CTG CGA CCC CCG CCC	576
	Ala Leu Cys Ala Leu Gly Gly Pro Gly Leu Arg Pro Pro Pro	
	15 20 25	
35	GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG	624
	Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln	
	30 35 40 45	
	CGC GAG ATC CTG GCG GTG CTC GGG CCT GGG CGG CCC CGG CCC CGC	672
	Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg	
	50 55 60	
40	GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
	Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
	65 70 75	
45	CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAG GAC GGC GCG	768
	Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
	80 85 90	

50

55

	CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val 95 100 105	816
5	AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp 110 115 120 125	864
10	AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val 130 135 140	912
15	ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu 145 150 155	960
20	AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser 160 165 170	1008
25	AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT Asn Arg Glu Ser Asp Leu Phe Leu Asp Leu Gln Thr Leu Arg Ala 175 180 185	1056
30	GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys 190 195 200 205	1104
35	TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu 210 215 220	1152
40	ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly 225 230 235	1200
45	CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg 240 245 250	1248
50	GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg 255 260 265	1296
55	AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC AAC CGA CTC Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu 270 275 280 285	1344
55	CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG GTC TGC Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys 290 295 300	1392

	CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG CTG GAC Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp 305 310 315	1440
5		
	TGG GTC ATC GCT CCC CAA GGC TAC TCG GCC TAT TAC TGT GAG GGG GAG Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu 320 325 330	1488
10		
	TGC TCC TTC CCA CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC ATC Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile 335 340 345	1536
15		
	CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala 350 355 360 365	1584
20		
	TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp 370 375 380	1632
25		
	AGC AGC AAC AAC GTC ATC CTG CGC AAA CAC CGC AAC ATG GTG GTC AAG Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys 385 390 395	1680
30	(2) INFORMATION FOR SEQ ID NO:21:	

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

- (A) OTHER INFORMATION: /product= "hOP2-PP"

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:21:

45	Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys 1 5 10 15	
50	Ala Leu Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro 20 25 30	
	Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile 35 40 45	

55

Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
 50 55 60

5 Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
 65 70 75 80

Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
 10 85 90 95

Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
 100 105 110

15 Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
 115 120 125

Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala
 130 135 140

20 Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr
 145 150 155 160

Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu
 25 165 170 175

Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu
 180 185 190

Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu
 30 195 200 205

Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp
 210 215 220

35 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala
 225 230 235 240

Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro
 245 250 255

40 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln
 260 265 270

Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile
 275 280 285

45 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His
 290 295 300

50 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile
 305 310 315 320

Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335
 5 Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 340 345 350
 10 Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365
 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380
 15 Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400
 Cys His

20 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE; cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

35 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 93..1289
- (D) OTHER INFORMATION: /note= "mOP2 cDNA"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

45	GCCAGGCACA GGTGCGCCGT CTGGTCCTCC CCGTCTGGCG TCAGCCGAGC	50
	CCGACCAAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT	104
	Met Ala Met Arg	
	1	
50	CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC	152
	Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly	
	5 10 15 20	
55	GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA	200
	Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly	
	25 30 35	

	GGC CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly 40 45 50	248
5	CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln 55 60 65	296
10	CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr 70 75 80	344
15	GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp 85 90 95 100	392
20	CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly 105 110 115	440
25	TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile 120 125 130	488
30	CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu 135 140 145	536
35	CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu 150 155 160	584
40	GTG GTC CAA GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp 165 170 175 180	632
45	CTT CAG ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG CTG GAC ATC Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile 185 190 195	680
50	ACA GCA GCC AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GGA Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly 200 205 210	728
	CTC CGC CTC TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT CCT GGC Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly 215 220 225	776
	CTG GCT GGT CTG CTT GGA CGA CAA GCA CCA CGC TCC AGA CAG CCT TTC Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe 230 235 240	824

	ATG GTA ACC TTC TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT CGG Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg 245 250 255 260	872
5	GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA AAG AAA ACG AAC GAG CTT Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu 265 270 275	920
10	CCG CAC CCC AAC AAA CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser 280 285 290	968
15	CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC TAC GTC AGC TTC CGT Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg 295 300 305	1016
20	GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala 310 315 320	1064
25	TAT TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC TCC TGT ATG AAC Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn 325 330 335 340	1112
30	GCC ACC AAC CAT GCC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro 345 350 355	1160
35	GAT GTT GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GCC ACC Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr 360 365 370	1208
40	TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His 375 380 385	1256
45	CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCG CCCAGCATCC Arg Asn Met Val Val Lys Ala Cys Gly Cys His 390 395	1309
50	TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAC CCTTCTATGT TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCCTGCTA AAATTCTGGT CTTCCTCCAGT TCCTCTGTCC TTCAATGGGT TTGGGGCTA TCACCCCCGCC CTCTCCATCC TCCTACCCCA AGCATAGACT GAATCCACAC AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC CTCAGCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAAATTC TAAACTAGAT	1369 1429 1489 1549 1609 1669

5	GATCTGGGCT CTCTGCACCA TTCAATTGGG CAGTTGGGAC ATTTTAGGT ATAACAGACA	1729
	CATACACTTA GATCAATGCA TCCCTGTACT CCTTGAATTC AGAGCTAGCT TGTTAGAAA	1789
	AGAACATCAGAG CCAGGTATAG CGGTGCATGT CATTAAATCCC AGCGCTAAAG AGACAGAGAC	1849
	AGGAGAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAAA	1909
10	AAAAAAAAAAC CGAATTTC	1926

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iv) FEATURE:

(D) OTHER INFORMATION: /product= "mOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

30

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Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met
 150 155 160
 5 Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe
 165 170 175
 Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu
 180 185 190
 10 Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp
 195 200 205 210
 15 Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
 215 220 225
 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln
 230 235 240
 20 Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala
 245 250 255
 Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn
 260 265 270
 25 Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His
 275 280 285 290
 Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser
 295 300 305
 30 Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr
 310 315 320
 Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
 325 330 335
 Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
 340 345 350
 40 Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
 355 360 365 370
 Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
 375 380 385
 45 Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
 390 395

50 (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..1368
(D) OTHER INFORMATION:/STANDARD NAME="60A"

(x) PUBLICATION INFORMATION:

(A) AUTHORS: VHARTON, KRISTI A.; THOMSEN, GERALD H.; GELBERT, WILLIAM M.
(B) TITLE: DROSOPHILA 60A GENE...
(C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
(D) VOLUME: 88
(E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
(F) PAGES: 9214-9218
(G) DATE: OCT - 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser	48
1 5 10 15	
CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GCG ACC ACG CCG CCG Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	96
20 25 30	
GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GCC AAG GAC Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	144
35 40 45	
CAG ACG ATC ATG CAC AGA GTG CTG AGC GAG GAC GAC AAG CTG GAC GTC Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	192
50 55 60	
TCG TAC GAG ATC CTC GAG TTC CTG GCC ATC GAA CGG CCG ACG CAC Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	240
65 70 75 80	
CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCC AAG TTC CTG Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	288
85 90 95	

	CTG GAC GTC TAC CAC CGC ATC ACG GCG GAG GAG GGT CTC AGC GAT CAG Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln 100 105 110	336
5	GAT GAG GAC GAC GAC TAC GAA CGC GGC CAT CGG TCC AGG AGG AGC GCC Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala 115 120 125	384
10	GAC CTC GAG GAG GAT GAG GGC GAG CAG CAG AAG AAC TTC ATC ACC GAC Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp 130 135 140	432
15	CTG GAC AAG CGG GCC ATC GAC GAG AGC GAC ATC ATC ATG ACC TTC CTG Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu 145 150 155 160	480
20	AAC AAG CGC CAC CAC AAT GTG GAC GAA CTG CGT CAC GAG CAC GGC CGT Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg 165 170 175	528
25	CGC CTG TGG TTC GAC GTC TCC AAC GTG CCC AAC GAC AAC TAC CTG GTG Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asn Tyr Leu Val 180 185 190	576
30	ATG GCC GAG CTG CGC ATC TAT CAG AAC GCC AAC GAG GGC AAG TGG CTG Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu 195 200 205	624
35	ACC GCC AAC AGG GAG TTC ACC ATC ACG GTA TAC GCC ATT GGC ACC GGC Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly 210 215 220	672
40	ACG CTG GGC CAG CAC ACC ATG GAG CCG CTG TCC TCG GTG AAC ACC ACC Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr 225 230 235 240	720
45	GGG GAC TAC GTG GGC TGG TTG GAG CTC AAC GTG ACC GAG GGC CTG CAC Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His 245 250 255	768
50	GAG TGG CTG GTC AAG TCG AAG GAC AAT CAT GGC ATC TAC ATT GGA GCA Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala 260 265 270	816
	CAC GCT GTC AAC CGA CCC GAC CGC GAG GTG AAG CTG GAC GAC ATT GGA His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly 275 280 285	864
	CTG ATC CAC CGC AAG GTG GAC GAC GAG TTC CAG CCC TTC ATG ATC GGC Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly 290 295 300	912

	TTC TTC CGC GGA CCG GAG CTG ATC AAG GCG ACG GCC CAC AGC AGC CAC Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His 305 310 315 320	960
5	CAC AGG AGC AAG CGA AGC GCC AGC CAT CCA CGC AAG CGC AAG AAG TCG His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser 325 330 335	1008
10	GTC TCG CCC AAC AAC GTG CCG CTG CTG GAA CCG ATG GAG AGC ACG CGC Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg 340 345 350	1056
15	AGC TGC CAG ATG CAG ACC CTG TAC ATA GAC TTC AAG GAT CTG GGC TGG Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp 355 360 365	1104
20	CAT GAC TGG ATC ATC GCA CCA GAG GGC TAT GGC GCC TTC TAC TGC AGC His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser 370 375 380	1152
25	GGC GAG TGC AAT TTC CCG CTC AAT GCG CAC ATG AAC GCC ACG AAC CAT Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His 385 390 395 400	1200
30	GCG ATC GTC CAG ACC CTG GTC CAC CTG CTG GAG CCC AAG AAC CTG CCC Ala Ile Val Gln Thr Leu Val His Leu Glu Pro Lys Lys Val Pro 405 410 415	1248
35	AAG CCC TGC TGC GCT CCG ACC AGG CTG GGA GCA CTA CCC GTT CTG TAC Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr 420 425 430	1296
40	CAC CTG AAC GAC GAG AAT GTG AAC CTG AAA AAG TAT AGA AAC ATG ATT His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile 435 440 445	1344
	GTC AAA TCC TGC GGG TGC CAT TGA Val Lys Ser Cys Gly Cys His 450	1368

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

50

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Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
 1 5 10 15
 5 Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro
 20 25 30
 Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp
 35 40 45
 10 Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val
 50 55 60
 Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His
 65 70 75 80
 15 Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu
 85 90 95
 20 Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln
 100 105 110
 Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala
 115 120 125
 25 Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp
 130 135 140
 Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu
 145 150 155 160
 30 Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg
 165 170 175
 Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val
 35 180 185 190
 Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu
 195 200 205
 Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly
 40 210 215 220
 Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr
 225 230 235 240
 45 Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His
 245 250 255
 50 Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala
 260 265 270

His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly
 275 280 285
 5 Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly
 290 295 300
 Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His
 305 310 315 320
 10 His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Ser
 325 330 335
 Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg
 15 340 345 350
 Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
 355 360 365
 20 His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
 370 375 380
 Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 385 390 395 400
 25 Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
 405 410 415
 Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
 420 425 430
 30 His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
 435 440 445
 35 Val Lys Ser Cys Gly Cys His
 450 455

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein
 (iii) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

50 (ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note="BMP3"

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i)SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein
 (ix) FEATURE:

10

(A) NAME/KEY: Protein
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

15

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
 1 5 10 15

20

Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Try Cys Ser Gly
 20 25 30

Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
 35 40 45

25

Thr Ile Gln Ser Ile Val Ala Arg Ala Val Gly Val Val Pro Gly Ile
 50 55 60

30

Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
 65 70 75 80

35

Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
 85 90 95

Thr Val Glu Ser Cys Ala Cys Arg
 100

35

(2) INFORMATION FOR SEQ ID NO:27:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

50

(ix) FEATURE:

(A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note= "BMP5"

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 1 5 10 15

5 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 20 25 30

10 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45

15 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 50 55 60

20 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80

25 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 85 90 95

30 Arg Ser Cys Gly Cys His
 100

(2) INFORMATION FOR SEQ ID NO:28:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein
 (vi) ORIGINAL SOURCE:

35 (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

45 Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln
 1 5 10 15

50

55

Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly
 20 25 30

5 Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 35 40 45

10 Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu Tyr Val Pro Lys
 50 55 60

15 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 65 70 75 80

20 Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Trp Met Val Val
 85 90 95

25 Arg Ala Cys Gly Cys His
 100

20 (2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30 (ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /label= OPX /note= "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY SELECTED FROM THE RESIDUES OCCURRING AT THE CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or 16,18,20 and 22.)"

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
 1 5 10 15

45 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
 20 25 30

Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
 35 40 45

50 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
 50 55 60

Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
 65 70 75 80

Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
 85 90 95

Xaa Ala Cys Gly Cys His
 100

10

(2) INFORMATION FOR SEQ ID NO:30:

(i)SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

20

(ii)MOLECULE TYPE: protein

(ix)FEATURE:

- (A) NAME: Generic Sequence 5

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

25

(xi)SEQUENCE DESCRIPTION: SEQ ID NO:30:

30

Leu Xaa Xaa Xaa Phe
 1 5
 Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 10
 Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 15 20
 Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 25 30
 Xaa Pro Xaa Xaa Xaa Xaa Xaa
 35
 Xaa Xaa Xaa Asn His Ala Xaa Xaa
 40 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55 60
 Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 65
 Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70 75
 Xaa Xaa Xaa Val Xaa Leu Xaa
 80
 Xaa Xaa Xaa Met Xaa Val Xaa
 85 90
 Xaa Cys Xaa Cys Xaa
 95

50

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(2) INFORMATION FOR SEQ ID NO:31:

(i)SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein
(ix) FEATURE:

(A) NAME: Generic Sequence 6
(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

15	Cys Xaa Xaa Xaa Iaa Leu Xaa Xaa Xaa Phe
	1 5 10
	Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
	15
20	Iaa Xaa Pro Xaa Xaa Xaa Xaa Ala
	20 25
	Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
	30 35
	Xaa Pro Xaa Xaa Xaa Xaa Xaa
	40
	Xaa Xaa Xaa Asn His Ala Xaa Xaa
	45 50
25	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
	55
	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
	60 65
	Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
	70
30	Xaa Xaa Xaa Leu Xaa Xaa Xaa
	75 80
	Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
	85
	Iaa Xaa Xaa Xaa Met Xaa Val Xaa
	90 95
35	Xaa Cys Xaa Cys Xaa
	100

(2) INFORMATION FOR SEQ ID NO:32:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1238 base pairs, 372 amino acids
- (B) TYPE: nucleic acid, amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) ORIGINAL SOURCE:

50 (A) ORGANISM: human

55 (iv) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:
(D) OTHER INFORMATION: /product= "GDE-1" /note= "GDE-1 cDNA"

(x) PUBLICATION INFORMATION:

5
 (A) AUTHORS: Lee, Se-Jin
 (B) TITLE: Expression of Growth/Differentiation Factor 1
 (C) JOURNAL: Proc. Nat'l Acad. Sci.
 (D) VOLUME: 88
 (E) RELEVANT RESIDUES: 1-1238
 (F) PAGES: 4250-4254
 (G) DATE: May-1991

10
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

15	GGGGACACCG GCCCCGCCCT CAGCCCACTG GTCCCCGGGCC GCCGC GGACC CTGCCCACTC	60
	TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC	
	Met Pro Pro Pro Gln Gln Gly Pro Cys Gly	
	1 5 10	
20	CAC CAC CTC CTC CTC CTC CTG GCC CTG CTG CTG CCC TCG CTG CCC	158
	His His Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro	
	15 20 25	
25	CTG ACC CGC GCC CCC GTG CCC CCA GGC CCA GCC GCC GCC CTG CTC	203
	Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu	
	30 35 40	
	CAG GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCC CCC AGG CTC	248
	Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu	
	45 50 55	
30	CGG CCG GTT CCC CCG GTC ATG TGG CGC CTG TTT CGA CGC CGG GAC	293
	Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp	
	60 65 70	
35	CCC CAG GAG ACC AGG TCT GGC TCG CGG CGG ACG TCC CCA GGG GTC	338
	Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val	
	75 80 85	
40	ACC CTG CAA CCG TGC CAC GTG GAG GAG CTG GGG GTC GCC GGA AAC	383
	Thr Leu Gln Pro Cyc His Val Glu Glu Leu Gly Val Ala Gly Asn	
	90 95 100	

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	ATC GTG CGC CAC ATC CCG GAC CGC GGT GCG CCC ACC CGG GCC TCG Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser 105 110 115	428
5	GAG CCT GTC TCG GCC GCG GGG CAT TGC CCT GAG TGG ACA GTC GTC Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val 120 125 130	473
10	TTC GAC CTG TCG GCT GTG GAA CCC GCT GAG CGC CCG AGC CGG GCC Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala 135 140 145	518
15	CGC CTG GAG CTG CGT TTC GCG GCG GCG GCG GCA GCC CCG GAG Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu 150 155 160	563
20	GCG GGC TGG GAG CTG AGC GTG GCG CAA GCG GGC CAG GGC GCG GGC Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly 165 170 175	608
25	GCG GAC CCC GGG CCG GTG CTG CTC CGC CAG TTG GTG CCC GCC CTG Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu 180 185 190	653
30	GGG CCG CCA GTG CGC GCG GAG CTG CTG GGC GCC GCT TGG GCT CGC Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg 195 200 205	698
35	AAC GCC TCA TGG CCG CGC AGC CTC CGC CTG GCG CTG GCG CTA CGC Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg 210 215 220	743
40	CCC CGG GCC CCT GCC GCC TGC GCG CGC CTG GCC GAG GCC TCG CTG Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu 225 230 235	788
45	CTG CTG GTG ACC CTC GAC CCG CGC CTG TGC CAC CCC CTG GCC CGG Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg 240 245 250	833
50	CCG CGG CGC GAC GCC GAA CCC GTG TTG GGC GGC GGC CCC GGG GGC Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Pro Gly Gly 255 260 265	878
55	GCT TGT CGC CGG CGG CGG CTG TAC GTG AGC TTC CGC CAG GTG GGC Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly 270 275 280	923
55	TGG CAC CGC TGG GTC ATC GCG CCG CGC CCC TTC CTG GCC AAC TAC Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr 285 290 295	968

	TGC CAG GGT CAG TGC GCG CTG CCC GTC GCG CTG TCG GGG TCC GGG Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly 300 305 310	1013
5	GGG CCG CCG GCG CTC AAC CAC GCT GTG CTG CGC GCG CTC ATG CAC Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His 315 320 325	1058
10	GCG GCC CCC CCG GGA GCC GCC GAC CTG CCC TGC TGC GTG CCC GCG Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala 330 335 340	1103
15	GCG CTG TCG CCC ATC TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn 345 350 355	1148
	GTG GTG CTG CCG CAG TAT GAG GAC ATG GTG GTG GAC GAG TGC GGC Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly 360 365 370	1193
20	TGC CGC TAACCCGGGG CGGGCACCGA CCCGGGCCCA ACAATAATG CCGCGTGG 1238 Cys Arg 372	

25 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (F) TISSUE TYPE: BRAIN

45 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:
- (D) OTHER INFORMATION: /function= /product= "GDF-1"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

	Met Pro Pro Pro Gln Gln Gly Pro Cys Gly
55	1 5 10

	His His Leu Leu Leu Leu Ala Leu Leu Pro Ser Leu Pro		
	15	20	25
5	Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu		
	30	35	40
	Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu		
10	45	50	55
	Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp		
	60	65	70
15	Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val		
	75	80	85
	Thr Leu Gln Pro Cyc His Val Glu Glu Leu Gly Val Ala Gly Asn		
	90	95	100
20	Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser		
	105	110	115
	Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val		
25	120	125	130
	Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala		
	135	140	145
	Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Pro Glu		
30	150	155	160
	Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly		
	165	170	175
35	Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu		
	180	185	190
	Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg		
40	195	200	205
	Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg		
	210	215	220
	Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu		
45	225	230	235
	Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg		
	240	245	250
50	Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly		
	255	260	265

Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly
 270 275 280
 5 Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr
 285 290 295
 10 Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly
 300 305 310
 Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His
 315 320 325
 15 Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala
 330 335 340
 Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn
 345 350 355
 20 Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly
 360 365 370
 25 Cys Arg
 372

Claims

30 1. Use of a morphogen selected from the group consisting of OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16; or a morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal (eg a human) and comprises a pair of folded polypeptides, the amino acid sequence of each of which comprises

35 (a) the sequence of the seven cysteine domain of human OP-1, mouse OP-1, human OP-2, mouse OP-2 or 60A; or
 (b) an amino acid sequence selected from Seq. ID Nos 9, 10, 11, 12, 13, 14, 26, 27, 28 or 29 (CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx), GDF-1(fx), BMP3, BMP5, BMP6 or OPX), or
 40 (c) an amino acid sequence of residues 38-139 of Seq. ID Nos. 5, 6, 7 or 8 or residues 354-455 of Seq ID No. 24.

for the manufacture of a medicament for:

45 (a) modulating an inflammatory response; or
 (b) alleviating the tissue destructive effects associated with the inflammatory response to tissue injury; or

2. Use according to claim 1 for modulating an inflammatory response in mammalian tissue, wherein the modulation of said inflammatory response comprises:

50 (a) alleviation of fibrosis or scar tissue formation; and/or
 (b) inhibition of adherence of immune effector cells to vascular endothelium; and/or
 (c) alleviation of interstitial inflammation; and/or
 (d) alleviation of edema or erythema; and/or
 (e) alleviation of inflammatory tissue necrosis.

55 3. Use according to claim 1 or claim 2 wherein the inflammatory response is associated with tissue injury (the injury for example being chemically, mechanically, biologically or immunologically related).

4. Use according to any one of the preceding claims wherein said medicament is administered: (a) for the treatment or prophylaxis of said tissue injury; and/or (b) in an amount effective to inhibit fibrogenesis or stimulate tissue-specific regeneration of said injured or damaged tissue; and/or (c) to inhibit loss or reduction of function of said tissue; and/or (d) orally, parenterally or topically; and/or (e) dispersed in a liquid tissue adhesive; and/or (f) in an aerosol.

5

5. Use according to claim 3 or 4 wherein said tissue injury includes:

10 (a) ischaemic-reperfusion injury; or
 (b) hyperoxia injury.

6. Use according to claim 5(a) wherein said ischaemic-reperfusion injury is:

15 (a) associated with cardiac arrest, pulmonary occlusion, arterial (eg renal artery) occlusion, coronary occlusion or occlusive stroke; or
 (b) associated with surgery or the reduction or interruption of blood flow to an organ in a clinical procedure (eg carotid endarterectomy, coronary artery bypass, a tissue grafting procedure, an organ transplant or fibrinolytic therapy); or
 (c) associated with cerebral infarction, myocardial infarction, asphyxia or cardiopulmonary arrest.

20

7. Use according to claim 5(b) wherein the hyperoxia injury is associated with the treatment of:

25 (a) a prematurely newborn baby; or
 (b) emphysema; or
 (c) asphyxia.

8. Use according to any one of the preceding claims wherein the tissue is lung, cardiac, hepatic, neural, pancreatic, synovial, skin or renal tissue, for example wherein:

30 (a) the tissue is renal tissue and the mammal is afflicted with glomerular nephritis, atherosclerosis or diabetes, or
 (b) the tissue is cardiac tissue and the mammal is afflicted with atherosclerosis or vascular disease, or
 (c) the tissue is pancreatic tissue and the mammal is afflicted with diabetes, or
 (d) the tissue is synovial tissue and the mammal is afflicted with arthritis,
 (e) the tissue is skin tissue and the mammal is afflicted with dermatitis or psoriasis,
 (f) the tissue is lung tissue and the mammal is afflicted with bronchitis, emphysema, idiopathic pulmonary fibrosis, asthma, asphyxia, or adult respiratory distress syndrome.

35

9. Use according to claim 3 or 4 wherein the tissue injury includes:

40 (a) an immune-cell mediated inflammatory response; or
 (b) an inflammatory disease (eg a chronic inflammatory disease); or
 (c) an abnormal immune response; or
 (d) edema or erythema.

45

10. Use according to claim 9(a), 9(c) or 9(d) wherein the tissue injury includes:

50 (a) a generalized acute inflammatory response; or
 (b) airway inflammation.

55

11. Use according to claim 9(b) wherein the inflammatory disease includes:

(a) an autoimmune disease; or
 (b) arthritis, psoriasis, dermatitis, inflammatory bowel disease or diabetes.

12. Use according to claim 10 wherein:

(a) in claim 10(a) the acute inflammatory response is associated with asphyxia or adult respiratory distress

syndrome; or
 (b) in claim 10(b) the airway inflammation is associated with chronic bronchitis, emphysema, idiopathic pulmonary fibrosis or asthma.

5 13. Use according to claim 11 wherein:

(a) in claim 11(a) the autoimmune disease is a neurodegenerative disease (eg multiple sclerosis or amyotrophic lateral sclerosis); or
 (b) in claim 11(b) the arthritis is rheumatoid, degenerative or psoriatic arthritis.

10 14. Use according to any one of claims 3-13 wherein the modulation of the inflammatory response is effected by administration of the medicament before or after the injury, for example prior to or after the reduction or interruption of blood flow or after resumption of blood flow when the injury is ischaemic-reperfusion injury.

15 15. Use according to claim 6(b) wherein said clinical procedure is a tissue grafting procedure (eg of skin, bone marrow or gastrointestinal mucosa tissue) or an organ transplant procedure (eg of lung, heart, kidney, liver or pancreas).

16. Use according to claim 15 wherein the modulation of the inflammatory response is effected by administration of the medicament:

20 (a) upon or following removal of the organ or tissue from a donor host; or
 (b) during storage or transportation of the organ or tissue prior to implantation into a recipient host; or
 (c) upon or following implantation into a recipient host.

25 17. Use according to any one of the preceding claims wherein said medicament comprises the morphogen dispersed in a physiologically acceptable aqueous carrier suitable for parenteral administration to a mammal.

30 18. A pharmaceutical composition for use in alleviating injury associated with exposure of mammalian tissue to toxic oxygen concentrations, comprising a morphogen dispersed in a physiologically acceptable aqueous carrier to a concentration effective for alleviating extravasation of immune effector cells, interstitial inflammation, edema, necrosis or fibrogenesis in mammalian tissue at risk of, or afflicted with, said injury, said morphogen selected from the group consisting of OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16; or said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq. ID No. 5), said composition further comprising a free oxygen radical inhibiting agent or an anticoagulant

35 19. A preservation solution for maintaining ex vivo viability of mammalian cells or tissue or a mammalian organ, comprising a fluid formulation having an osmotic pressure substantially equivalent to the osmotic pressure of living mammalian cells and a morphogen dispersed in said fluid to a concentration effective for alleviating extravasation of immune effector cells, interstitial inflammation, edema, necrosis or fibrogenesis in said cells, tissue or organ, said morphogen selected from the group consisting of OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16; or said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises the C-terminal seven cysteine domain of human OP-1 (residues 38-139 of Seq. ID No. 5).

40 20. A solution according to claim 19, further comprising a sugar, an anticoagulant or a free oxygen radical inhibiting agent; or, further formulated to maintain substantially normal ATP levels in said cells, tissue or organ.

45 21. The composition of claim 18 or the solution of claim 19 or 20 wherein the morphogen is as defined in claim 1.

50 22. An ex vivo method for protecting a living mammalian tissue or transplanted mammalian organ from injury associated with the inflammatory response of activated immune effector cells comprising the step of providing to said tissue or organ a morphogen selected from the group consisting of OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16; or said morphogen comprising a dimeric protein that induces tissue-specific morphogenesis in a mammal, said dimeric protein comprising a pair of folded polypeptides, the amino acid sequence of each of which comprises the C-terminal seven cysteine domain

of human OP-1 (residues 38-139 of Seq. ID No. 5).

23. The method of claim 22 wherein:

- 5 (a) the tissue or organ is as defined in claim 15; and/or
 (b) the morphogen is as defined in claim 1,
 (c) the morphogen is provided in the form of a solution as defined in claim 19 or 20.

10 Patentansprüche

1. Verwendung eines Morphogens, das aus der Gruppe ausgewählt ist, die aus OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16 besteht; oder eines Morphogens, das ein dimeres Protein umfaßt, das bei einem Säugetier (beispielsweise einem Menschen) eine gewebsspezifische Morphogenese induziert und zwei gefaltete Polypeptide umfaßt, wobei die Aminosäure-Sequenz von jedem folgendes umfaßt:

- (a) die Sequenz der Sieben-Cystein-Domäne von menschlichem OP-1, Maus OP-1, menschlichem OP-2, Maus OP-2 oder 60A; oder
- (b) eine Aminosäure-Sequenz, die aus den Sequenz ID Nr. 9, 10, 11, 12, 13, 14, 26, 27, 28 oder 29 (CBMP2A (fx), CBMP2B(fx), DPP(fx), Vgr-1(fx), GDF-1(fx), BMP3, BMP5, BMP6 oder OPX) ausgewählt ist; oder
- (e) eine Aminosäure-Sequenz der Reste 38-139 von Sequenz ID Nr. 5, 6, 7 oder 8 oder der Reste 354-455 von Sequenz ID Nr. 24; zur Herstellung eines Medikamentes zur:

- (a) Modulierung einer Entzündungsreaktion; oder
- (b) Verminderung der Gewebs-zerstörenden Wirkungen, die mit der Entzündungsreaktion auf eine Gewebsschädigung verbunden sind.

2. Verwendung nach Anspruch 1 zur Modulierung einer Entzündungsreaktion in Säugetierge webe, wobei die Modulation der Entzündungsreaktion folgendes umfaßt:

- (a) Verminderung einer Fibrose oder Narbengewebsbildung; und/oder
- (b) Hemmung der Anhaftung von Immuneffektorzellen an vaskuläres Endothel; und/oder
- (c) Verminderung einer interstitiellen Entzündung; und/oder
- (d) Verminderung eines Ödems oder Erythems; und/oder
- (e) Verminderung einer entzündlichen Gewebsnekrose.

3. Verwendung nach Anspruch 1 oder Anspruch 2, bei der die Entzündungsreaktion mit einer Gewebsschädigung verbunden ist (wobei die Verletzung beispielsweise chemisch, mechanisch, biologisch oder immunologisch verursacht ist).

4. Verwendung nach einem der vorhergehenden Ansprüche, bei der das Medikament:

- (a) zur Behandlung oder Prophylaxe der Gewebsschädigung; und/oder
- (b) in einer Menge, die zur Hemmung einer Fibrogenese oder zur Stimulierung einer gewebsspezifischen Regeneration des verletzten oder geschädigten Gewebes wirksam ist; und/oder
- (c) zur Hemmung eines Verlustes oder einer Verminderung der Funktion des Gewebes; und/oder
- (d) oral, parenteral oder topisch; und/oder
- (e) in einem flüssigen Gewebsklebstoff dispergiert; und/oder
- (f) in einem Aerosol

verabreicht wird.

5. Verwendung nach Anspruch 3 oder Anspruch 4, bei der die Gewebsschädigung:

- (a) eine ischämische Reperfusions-Schädigung; oder
- (b) Hyperoxie-Schädigung

einschließt.

6. Verwendung gemäß Anspruch 5 (a), bei der die ischämische Reperfusions- Schädigung:
 - (a) mit Herzstillstand, Lungenarterienverschluß, Arterienverschluß (beispielsweise Nierenarterienverschluß), Koronararterienverschluß oder durch Okklusion verursachten Schlag verbunden ist; oder
 - (b) mit einem chirurgischen Eingriff oder der Verminderung oder Unterbrechung des Blutstromes zu einem Organ bei einem klinischen Verfahren (beispielsweise einer Carotis-Enterektomie, aorto-koronarem Bypass, einem Gewebetransplantationsverfahren, einer Organtranplantations- oder fibrinolytische Therapie) verbunden ist; oder
 - (c) mit einem Gehirninfarkt, Herzinfarkt, mit Asphyxie oder Herz-/Lungenstillstand verbunden ist.
7. Verwendung nach Anspruch 5 (b), bei der die Hyperoxie-Schädigung mit der Behandlung:
 - (a) eines frühgeborenen Säuglings; oder
 - (b) Emphysems; oder
 - (c) Asphyxie
- verbunden ist.
8. Verwendung nach einem der vorhergehenden Ansprüche, bei der das Gewebe Lungen-, Herz-, Leber-, Nerven-, Pankreas-, Synovial-, Haut- oder Nierengewebe ist, bei dem beispielsweise:
 - (a) das Gewebe Nierengewebe ist und das Säugetier an glomerulärer Nephritis, Arteriosklerose oder Diabetes leidet, oder
 - (b) das Gewebe Herzgewebe ist und das Säugetier an Arteriosklerose oder einer Gefäßerkrankung leidet, oder
 - (c) das Gewebe Pankreasgewebe ist und das Säugetier an Diabetes leidet, oder
 - (d) das Gewebe Synovialgewebe ist und das Säugetier an Arthritis leidet,
 - (e) das Gewebe Hautgewebe ist und das Säugetier an Dermatitis oder Psoriasis leidet,
 - (f) das Gewebe Lungengewebe ist und das Säugetier an Bronchitis, Emphysem, ideopathischer Lungenfibrose, Asthma, Asphyxie oder Schocklunge leidet.
9. Verwendung nach Anspruch 3 oder Anspruch 4, bei der die Gewebsverletzung:
 - (a) eine Immunzell-vermittelte Entzündungsreaktion; oder
 - (b) eine entzündliche Erkrankung (beispielsweise eine chronische entzündliche Erkrankung); oder
 - (c) eine abnormale Immunreaktion; oder
 - (d) ein Ödem oder Erythem einschließt.
10. Verwendung nach Anspruch 9 (a), 9 (c) oder 9 (d), bei der die Gewebsschädigung:
 - (a) eine generalisierte akute entzündliche Reaktion; oder
 - (b) Atemwegsentzündung
- einschließt.
11. Verwendung nach Anspruch 9 (b), bei der die entzündliche Erkrankung:
 - (a) eine Autoimmunerkrankung; oder
 - (b) Arthritis, Psoriasis, Dermatitis, eine entzündliche Darmerkrankung oder Diabetes
- einschließt.
12. Verwendung nach Anspruch 10, bei der:
 - (a) in Anspruch 10 (a) die akute entzündliche Reaktion mit Asphyxie oder Schocklunge verbunden ist; oder
 - (b) in Anspruch 10 (b) die Atemwegsentzündung mit chronischer Bronchitis, Emphysem, ideopathischer Lun-

genfibrose oder Asthma verbunden ist.

13. Verwendung nach Anspruch 11, bei der:

- 5 (a) in Anspruch 11 (a) die Autoimmunerkrankung eine neurodegenerative Erkrankung (beispielsweise Multiple Sklerose oder amyotrophe Lateralsklerose) ist; oder
- (b) in Anspruch 11 (b) die Arthritis eine rheumatoide, degenerative oder psoriatische Arthritis ist.

14. Verwendung nach einem der Ansprüche 3 bis 13, bei der die Modulation der Entzündungsreaktion durch Verabreichung des Medikaments vor oder nach der Schädigung, beispielsweise vor oder nach der Verringerung oder Unterbrechung des Blutstromes oder nach Wiederaufnahme eines Blutstromes verabreicht wird, wenn die Schädigung eine ischämische Reperfusions-Schädigung ist.

15. Verwendung nach Anspruch 6 (b), bei der das klinische Verfahren ein Gewebs-Transplantations-Verfahren (beispielsweise von Haut-, Knochenmark- oder Gewebe der Gastrointestinalschleimhaut) oder ein Organtransplantations-Verfahren (beispielsweise von Lunge, Herz, Niere, Leber oder Pankreas) ist.

16. Verwendung nach Anspruch 15, bei der die Modulation der Entzündungsreaktion durch Verabreichung des Medikamentes:

- 20 (a) bei oder im Anschluß an die Entfernung des Organs oder Gewebes von einem Spender; oder
- (b) während der Aufbewahrung oder des Transportes des Organs oder Gewebes vor Implantation in einen Empfänger; oder
- (c) bei oder im Anschluß an Implantation in einen Empfänger

25 bewirkt wird.

17. Verwendung nach einem der vorhergehenden Ansprüche, bei der das Medikament das das Morphogen in einem physiologisch akzeptablen wässrigen Träger, der zur parenteralen Verabreichung an ein Säugetier geeignet ist, dispergiert umfaßt.

18. Pharmazeutische Zusammensetzung zur Verwendung bei der Linderung einer Verletzung, die mit der Exposition von Säugetiergebebe gegenüber toxischen Sauerstoff--Konzentrationen verbunden ist, die ein Morphogen in einem physiologisch verträglichen wässrigen Träger in einer Konzentration dispergiert umfaßt, die zur Verminderung einer Extravasation von Immuneffektorzellen, einer interstitiellen Entzündung, eines Ödems, einer Nekrose oder einer Fibrogenese in säugetiergebebe wirksam ist, das dem Risiko der Schädigung ausgesetzt ist oder darunter leidet, wobei das Morphogen aus der Gruppe ausgewählt ist, die aus OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16 besteht; oder das Morphogen ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz jedes der beiden die C-terminale Sieben-Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) umfaßt, wobei die Zusammensetzung weiterhin ein Mittel zur Hemmung freier Sauerstoff-Radikale oder ein Antikoagulanz umfaßt.

45 19. Eine Konservierungslösung zur Aufrechterhaltung der ex vivo-Lebensfähigkeit von Säugetierzellen oder -gewebe oder eines Säugetierorgans, das eine flüssige Zubereitung umfaßt, die einen im wesentlichen dem osmotischen Druck lebender Säugetierzellen äquivalenten Druck und ein in der Flüssigkeit in einer Konzentration dispergiertes Morphogen aufweist, die zur Verminderung der Extravasation von Immuneffektorzellen, einer interstitiellen Entzündung, eines Ödems, einer Nekrose oder Fibrogenese bei diesen Zellen, Gewebe oder Organ wirksam ist, wobei das Morphogen aus der Gruppe ausgewählt ist, die aus OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16 besteht; oder das Morphogen ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz von jedem die C-terminale Sieben-Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) umfaßt.

55 20. Lösung nach Anspruch 19, die weiterhin einen Zucker, ein Antikoagulanz oder ein Mittel zur Hemmung freier Sauerstoff-Radikale umfaßt; oder weiterhin zur Aufrechterhaltung von im wesentlichen normalen ATP-Spiegeln in diesen Zellen, Gewebe oder Organ formuliert ist.

21. Zusammensetzung nach Anspruch 18 oder die Lösung nach Anspruch 19 oder 20, bei der das Morphogen wie in Anspruch 1 definiert ist.

22. Ex-vivo-Verfahren zum Schutz eines lebenden Säugetiergebietes oder transplantierten Säugetierorganen vor einer Schädigung, die mit der Entzündungsreaktion von aktivierten Immuneffektorzellen verbunden ist, das den Schritt umfaßt, dem Gewebe oder Organ ein Morphogen, das aus der Gruppe ausgewählt ist, die aus OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16 besteht; oder ein Morphogen zu verabreichen, das ein dimeres Protein umfaßt, das eine gewebsspezifische Morphogenese bei einem Säugetier induziert, wobei das dimere Protein zwei gefaltete Polypeptide umfaßt, und wobei die Aminosäure-Sequenz von jedem die C-terminale Sieben-Cystein-Domäne von menschlichem OP-1 (Reste 38-139 von Seq. ID Nr. 5) umfaßt.

23. Verfahren nach Anspruch 24, bei dem:

(a) das Gewebe oder Organ wie in Anspruch 15 definiert ist; und/oder
(b) das Morphogen wie in Anspruch 1 definiert ist; und/oder
(c) das Morphogen in der Form einer Lösung wie in Anspruch 19 oder 20 definiert verabreicht wird.

20 Revendications

1. Utilisation d'un morphogène choisi dans le groupe consistant en OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16 ou un morphogène comprenant une protéine dimère qui induit la morphogenèse tissu-spécifique chez un mammifère (par exemple un humain) et comprend une paire de polypeptides repliés, la séquence des acides aminés de chacun de ceux-ci comprenant:

(a) la séquence du domaine à sept cystéines de l'OP-1 humaine, OP-1 de souris, OP-2 humaine, OP-2 ou 60A de souris.
(b) une séquence d'acides aminés choisie parmi la séquence ID Nos. 9, 10, 11, 12, 13, 14, 26, 27, 28 ou 29 (CBMP2A(fx), CBMP2B(fx), DPP(fx), Vgl(fx), Vgr-1(fx), GDF-1(fx), BMP3, BMP5, BMP6 ou OPX); ou
(c) une séquence des acides aminés des résidus 38-139 de la séquence ID No. 5, 6, 7 ou 8 ou les résidus 354-455 de la séquence ID No. 24,

35 pour la fabrication d'un médicament pour:

(a) moduler une réponse inflammatoire; ou
(b) ralentir les effets de détérioration tissulaire associés à la réponse inflammatoire provoquée par une lésion tissulaire; ou
(c) accroître la viabilité des tissus lésés ou endommagés de mammifères (par exemple un tissu placé in vivo dans un mammifère).

2. Utilisation selon la revendication 1 pour moduler une réponse inflammatoire dans un tissu de mammifère, dans laquelle la modulation de cette réponse inflammatoire comprend:

(a) Le ralentissement de la formation des tissus fibrosés ou cicatriciels; et/ou
(b) l'inhibition de l'adhérence des cellules effectrices immunes sur l'endothélium vasculaire; et/ou
(c) le ralentissement d'une inflammation interstitielle; et/ou
(d) le ralentissement d'un oedème ou érythème; et/ou
(e) le ralentissement d'une nécrose des tissus inflammatoires.

3. Utilisation selon la revendication 1 ou la revendication 2 d'après laquelle la réponse inflammatoire est associée à une lésion tissulaire (la lésion étant par exemple liée à des causes chimiques, mécaniques, biologiques ou immunologiques).

4. Utilisation selon l'une quelconque des revendications précédentes dans laquelle ledit médicament est administré :
(a) pour le traitement ou la prophylaxie de ladite lésion tissulaire; et/ou (b) en une quantité efficace pour inhiber la fibrogénèse ou stimuler la régénération tissu-spécifique de ce tissu lésé ou endommagé; et/ou (c) pour inhiber

la perte ou la diminution de la fonction dudit tissu ; et/ou (d) par voie orale, parentérale ou topique; et/ou (e) dispersé dans un adhésif liquide tissulaire; et/ou (f) dans un aérosol.

5. Utilisation selon la revendication 3 ou 4 dans laquelle la dite lésion tissulaire comporte:

(a) une lésion ischémique par reperfusion; ou
(b) une lésion par hyperoxie.

6. Utilisation selon la revendication 5(a) dans laquelle la dite lésion ischémique par reperfusion est:

(a) associée à un arrêt cardiaque, une occlusion pulmonaire, une occlusion artérielle (par exemple d'une artère rénale), une occlusion d'une artère coronaire ou une attaque à caractère occlusif; ou
(b) associée à la chirurgie ou à la diminution ou à l'interruption de la circulation du sang vers un organe dans un traitement clinique (par exemple entérectomie de la carotide, un pontage d'une artère coronaire, un procédé de greffage d'un tissu, une transplantation d'organe ou une thérapie fibrinolytique); ou
(c) associée à un infarctus cérébral, un infarctus du myocarde, une asphyxie ou un arrêt cardio-pulmonaire.

7. Utilisation selon la revendication 5(b) dans laquelle la lésion à caractère hyperoxie est associée au traitement:

(a) d'un nouveau-né prématuré; ou
(b) d'un emphysème; ou
(c) d'une asphyxie.

8. Utilisation selon l'une quelconque des revendications précédentes d'après laquelle le tissu est un tissu pulmonaire, cardiaque, hépatique, neural, pancréatique, synovial, de la peau ou rénal, par exemple dans lequel:

(a) le tissu est un tissu rénal et le mammifère souffre d'une néphrite glomérulaire, d'athérosclérose ou d'un diabète, ou
(b) le tissu est un tissu cardiaque et le mammifère souffre d'une athérosclérose ou d'une maladie vasculaire, ou
(c) le tissu est un tissu pancréatique et le mammifère souffre du diabète, ou
(d) le tissu est un tissu synovial et le mammifère souffre d'arthrite,
(e) le tissu est un tissu de la peau et le mammifère souffre d'une dermatite ou d'un psoriasis,
(f) le tissu est un tissu du poumon et le mammifère souffre d'une bronchite, d'emphysème, de fibrose pulmonaire protopathique, d'asthme, d'asphyxie, ou du syndrome d'une douleur respiratoire de l'adulte.

9. Utilisation selon la revendication 3 ou 4 dans laquelle la lésion tissulaire comporte :

(a) une réponse inflammatoire à médiation de cellules immunitaires;
(b) une maladie inflammatoire (par exemple une maladie inflammatoire chronique); ou
(c) une réponse immunitaire anormale; ou
(d) un oedème ou un érythème.

10. Utilisation selon la revendication 9(a), 9(c), ou 9(d) dans laquelle la lésion tissulaire comporte:

(a) une réponse inflammatoire aiguë généralisée; ou
(b) une inflammation des voies aériennes.

11. Utilisation selon la revendication 9(b) d'après laquelle la maladie inflammatoire comporte :

(a) une maladie auto-immune; ou
(b) l'arthrite, un psoriasis, une dermatite, une maladie d'inflammation des intestins ou un diabète.

12. Utilisation selon la revendication 10 dans laquelle:

(a) dans la revendication 10(a) la réponse inflammatoire aiguë est associée à une asphyxie ou à un syndrome d'une douleur respiratoire de l'adulte; ou
(b) dans la revendication 10(b) l'inflammation de la voie aérienne est associée à une bronchite chronique, un emphysème, une fibrose pulmonaire protopathique ou à de l'asthme.

13. Utilisation selon la revendication 11 dans laquelle:

- (a) dans la revendication 11(a) la maladie auto-immune est une maladie neuro-dégénérative (par exemple une sclérose multiple ou une sclérose latérale amyotrophique); ou
- 5 (b) dans la revendication 11(b) l'arthrite est à caractère rhumatismal, dégénératif ou arthrite psoriasique.

14. Utilisation selon l'une quelconque des revendications 3-13 dans laquelle la modulation de la réponse inflammatoire est effectuée par l'administration d'un médicament avant ou après la lésion, par exemple avant ou après la réduction ou l'interruption de la circulation du sang ou après la reprise de la circulation du sang lorsque la lésion est une lésion ischémique par reperfusion.

15. Utilisation selon la revendication 6(b) dans laquelle la dite procédure clinique est un procédé de greffage d'un tissu (par exemple de peau, de moelle osseuse ou d'un tissu de la muqueuse gastro-intestinale) ou un procédé de transplantation d'un organe (par exemple d'un poumon, d'un cœur, d'un rein, d'un foie ou d'un pancréas).

16. Utilisation selon la revendication 15 d'après laquelle la modulation de la réponse inflammatoire est effectuée par l'administration du médicament:

- (a) dès ou après l'élimination de l'organe ou du tissu provenant d'un hôte donneur; ou
- 20 (b) pendant la conservation ou le transport de l'organe ou du tissu avant l'implantation chez un hôte receveur; ou
- (c) dès ou après l'implantation chez l'hôte receveur.

17. Utilisation selon l'une quelconque des revendications précédentes d'après laquelle ledit médicament comprend le morphogène dispersé dans un véhicule aqueux approprié physiologiquement acceptable pour une administration par voie parentérale à un mammifère.

18. Une composition pharmaceutique pour l'utilisation dans le ralentissement des lésions associées à une exposition d'un tissu d'un mammifère à des concentrations toxiques d'oxygène, comprenant un morphogène dispersé dans un véhicule aqueux physiologiquement acceptable à une concentration efficace pour ralentir l'extravasation des cellules effectrices immunes, un inflammation interstitielle, un oedème, une nécrose ou fibrogenèses dans un tissu de mammifère à risque, ou ayant souffert de, cette lésion, ledit morphogène choisi dans le groupe consistant en OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP4, COP-5, COP-7, COP-16 ou ce morphogène comprenant une protéine dimère qui induit une morphogenèse, tissu-spécifique chez un mammifère, cette protéine dimère comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celles-ci comprenant le domaine à sept cystéines du C-terminal de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5), la dite composition comprenant en outre un agent inhibant ou un anticoagulant à radical oxygène libre.

19. Une solution de conservation pour maintenir la viabilité ex vivo de cellules ou d'un tissu d'un mammifère ou d'un organe d'un mammifère, comprenant une formulation liquide possédant une pression osmotique essentiellement équivalente à la pression osmotique des cellules vivantes de mammifère et un morphogène dispersé dans ce liquide à une concentration efficace pour ralentir l'extravasation des cellules effectrices immunes, une inflammation interstitielle, un oedème, une nécrose ou fibrogenèses dans ces cellules , tissu ou organe, ce morphogène comprenant choisi dans le groupe consistant en OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP4, COP-5, COP-7, COP-16 ou ce morphogène une protéine dimère qui induit une morphogenèse tissu-spécifique chez un mammifère, ladite protéine dimère comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celles-ci comprend la séquence des acides aminés avec le C-terminal du domaine à sept cystéine de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5).

20. Une solution selon la revendication 19, comprenant en outre un sucre, un anticoagulant ou un agent inhibant à radical oxygène libre; ou, en outre formulé pour essentiellement maintenir les niveaux normaux d'ATP dans lesdites cellules, tissu ou organe.

21. Une composition selon la revendication 18 ou la solution selon la revendication 19 ou 20 dans laquelle le morphogène est tel que défini dans la revendication 1.

22. Une méthode ex vivo pour protéger un tissu vivant de mammifère ou un organe transplanté de mammifère contre

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des lésions associées à une réponse inflammatoire de cellules effectrices immunes activées comprenant l'étape de fournir au dit tissus ou organe un morphogène choisi dans le groupe consistant en OP-1, OP-2, BMP-5, BMP-6, BMP-2, BMP-4, Dpp, Vgl, Vgr-1, GDF-1, 60A, BMP-3, COP-1, COP-3, COP-4, COP-5, COP-7, COP-16 ou ce morphogène comprenant une protéine dimère qui induit une morphogenèse tissu-spécifique chez un mammifère,
5 la dite protéine dimère comprenant une paire de polypeptides repliés, la séquence des acides aminés de chacune de celle-ci comprend la séquence des acides aminés avec le domaine à sept cystéines du C-terminal de l'OP-1 humaine (résidus 38-139 de la séquence ID No.5).

23. La méthode selon la revendication 22 dans laquelle:

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(a) le tissu ou organe est tel que défini dans la revendication 15; et/ou
(b) le morphogène est tel que défini dans la revendication 1;
(c) le morphogène est fourni sous forme d'une solution telle que définie dans la revendication 19 ou 20.

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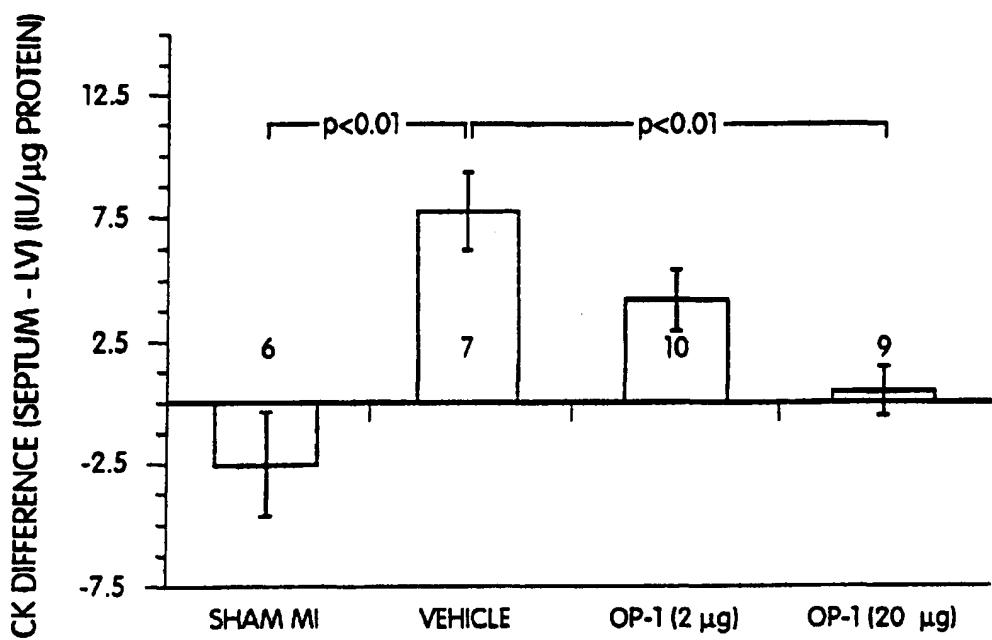


Fig. 1

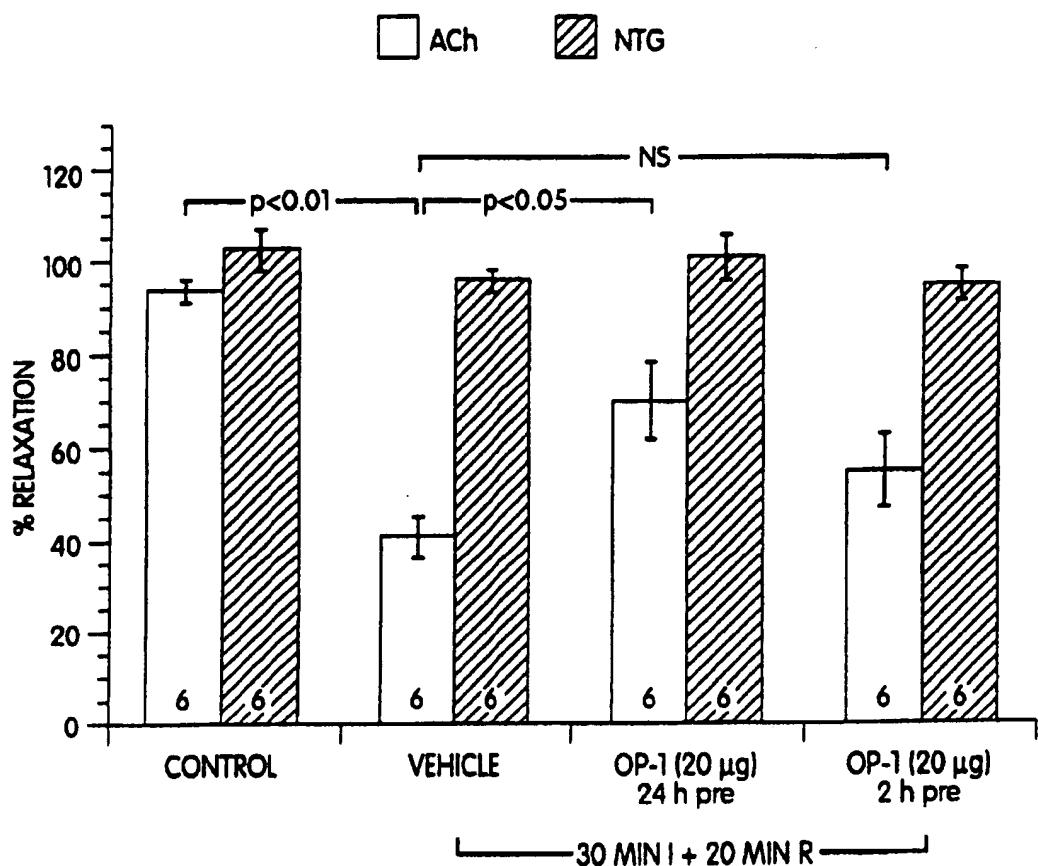


Fig 2

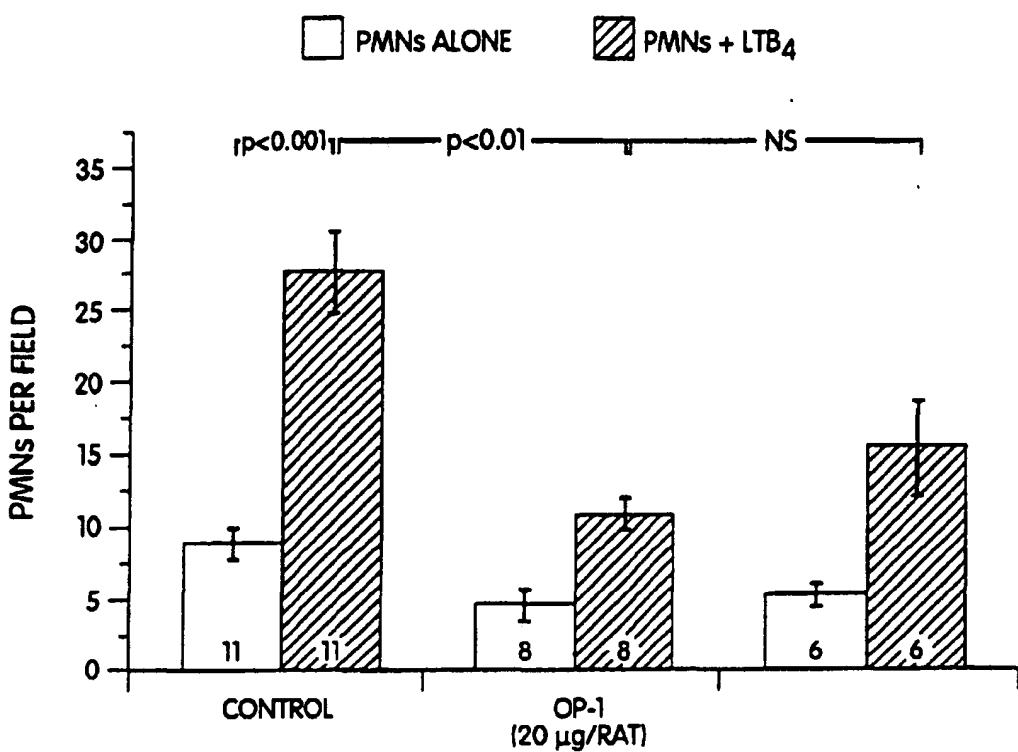


Fig. 3

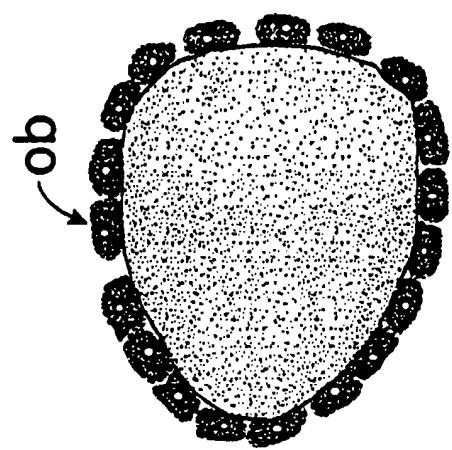


Fig. 4B

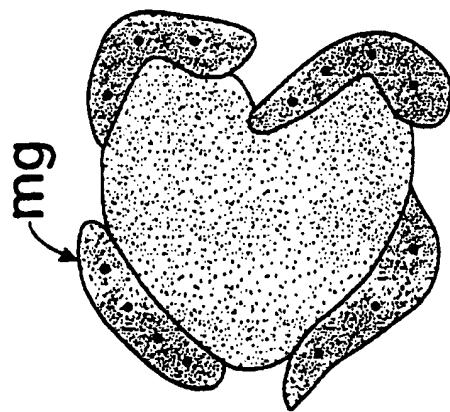


Fig. 4A

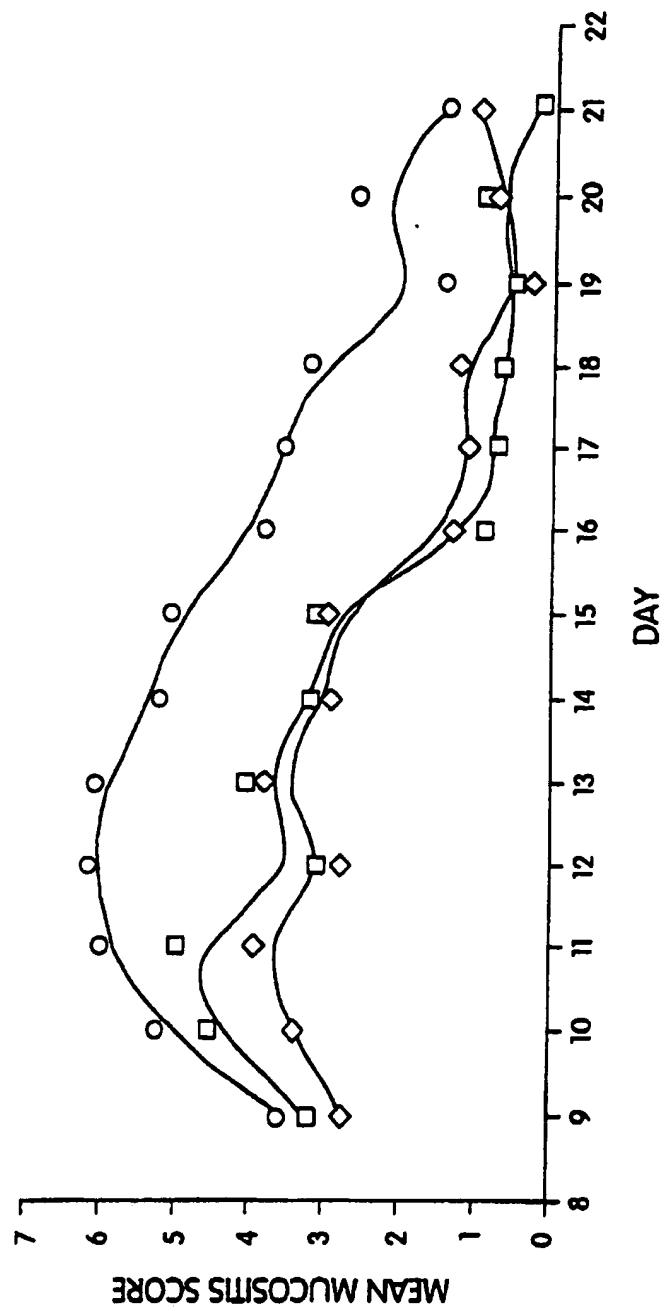


Fig. 5

Fig. 6A

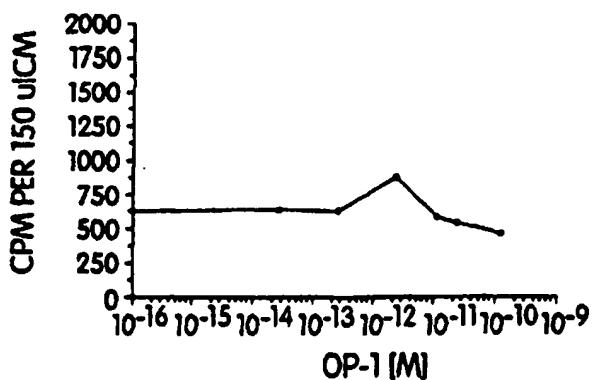


Fig. 6B

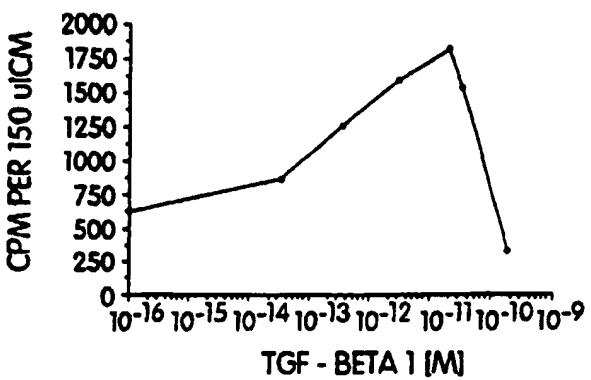


Fig. 6C

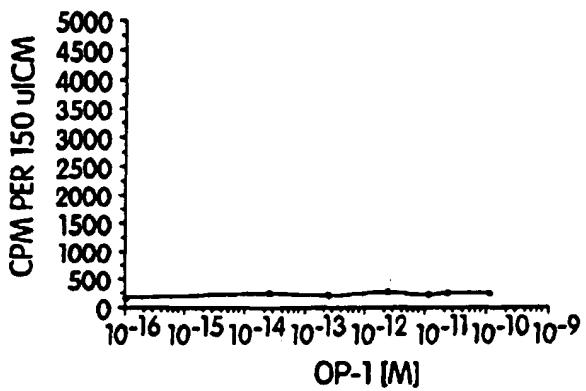


Fig. 6D

